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OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:06 ; Search time 25.17 seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-08-791-391A-32

Perfect score: 557
Sequence: 1 EVLQSPATLSLSPERAT.....CQSGSWPHTFGGKVKIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCFUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	90.8	107	1	US-07-634-278-63
2	506	90.8	107	1	US-07-634-278-87
3	506	90.8	107	1	US-08-477-728-63
4	506	90.8	107	1	US-08-477-728-87
5	506	90.8	107	1	US-08-474-040-63
6	506	90.8	107	1	US-08-474-040-87
7	506	90.8	107	1	US-08-487-200-63
8	506	90.8	107	1	US-08-487-200-87
9	506	90.8	107	4	US-08-484-537-63
10	506	90.8	107	4	US-08-484-537-87
11	480	86.2	127	2	US-08-476-176B-10
12	480	86.2	127	3	US-08-127-721A-10
13	480	86.2	127	3	US-08-485-246A-10
14	474	85.1	127	2	US-08-476-176B-6
15	474	85.1	127	3	US-08-127-721A-6
16	474	85.1	127	3	US-08-485-246A-6
17	473	84.9	107	2	US-08-232-081B-9
18	471	84.6	127	2	US-08-476-176B-8
19	471	84.6	127	3	US-08-127-721A-8
20	471	84.6	127	3	US-08-485-246A-8
21	449.5	80.7	107	3	US-08-783-853A-44
22	441	79.2	107	1	US-07-634-278-62
23	441	79.2	107	1	US-08-477-728-62
24	441	79.2	107	1	US-08-474-040-62
25	441	79.2	107	1	US-08-487-200-62
26	441	79.2	107	4	US-08-484-537-62
27	441	79.2	127	1	US-07-634-278-83

Sequence 83, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 4, Appl
Sequence 20, Appl
Sequence 4, Appl
Sequence 57, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 42, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60
DB 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60
QY 61 RFSGSGSGDTFTLTISRLPEDFAVYICQSSNSWPHFTFGGKVEIK 107
DB 61 RFSGSGSGDTFTLTISRLPEDFAVYICQSSNSWPHFTFGGKVEIK 107

RESULT 2

US-07-634-278-87
Sequence 87, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man-Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60
DB 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60
QY 61 RFSGSGSGDTFTLTISRLPEDFAVYICQSSNSWPHFTFGGKVEIK 107
DB 61 RFSGSGSGDTFTLTISRLPEDFAVYICQSSNSWPHFTFGGKVEIK 107

RESULT 3

US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60

Db 1 EIVLTQSPGTLISLGERATLSCRASQISNNLHWYQQKPGAPRLIIKYASQISGIPD 60
QY 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107
Db 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107

RESULT 4
US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-728-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQISNNLHWYQQKPGAPRLIIKYRQSGISGIPA 60
Db 1 EIVLTQSPGTLISLGERATLSCRASQISNNLHWYQQKPGAPRLIIKYASQISGIPD 60
QY 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107

Db 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107
RESULT 5
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQISNNLHWYQQKPGAPRLIIKYRQSGISGIPA 60
Db 1 EIVLTQSPGTLISLGERATLSCRASQISNNLHWYQQKPGAPRLIIKYASQISGIPD 60
QY 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107
Db 61 RESGSGGTDFTLTISLPEFAVYYCOQSGSWPHTFGGKVEIK 107

RESULT 7
US-08-487-200-63
; Sequence 63, Application US/08487200

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,200
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 87:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-487-200-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY	1	EIVLTQSPATLSLSPGERATISCAQASQSI	INHLHWYQRPQGPAPRLIIKYRSQSISGTPA	60
Db	1	EIVLTQSPGTLSPGERATISCRASQSI	INNLHWYQKQPGAPRLIIKYASQSISGIPD	60
QY	61	RFSGSGSGDFLTITSSLEPEDFAVYTCQSGSWPHTFGGKTVEIK	107	
Db	61	RFSGSGSGDFLTITSLRLEPEDFAVYTCQSGSNWPHTFGGTKVEIK	107	

RESULT 9
US-08-484-537-63
; Sequence 63, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCE ADDRESSES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,537
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PS-08-484-537-63

Query Match	90.8%	Score 506;	DB 4;	Length 107;
Best Local Similarity	90.7%;	Pred. No. 1e-40;		
Matches 97;	Conservative	3;	Mismatches 7;	Indels 0;
				Caps 0;

QY	1	EIVLTQSPATLSLSPGERATIS	SCQASQSI	SINHLHWYQOR	QCPARLLI	XYRQSISGIPA	60
Db	1	EIVLTQSPGTLSPGERATIS <th>SCRASQSI</th> <th>SINHLHWYQOK</th> <th>QCPARLLI</th> <th>XYRQSISGIPD</th> <th>60</th>	SCRASQSI	SINHLHWYQOK	QCPARLLI	XYRQSISGIPD	60
QY	61	RFGSGSGSDFTLTISSE	PEPDAFVYIQCSQSGSWPHPTFGG	TKVEIK	107		
Db	61	RFGSGSGSDFTLTISR	LEPEDAFVYIQCSQSGSWPHPTFGG	TKVEIK	107		

RESULT 10
US-08-484-537-87
; Sequence 87, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
;

; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-127-721a-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 3.2e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQISGIPA 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQISGTNIHWYQKPGQAPRLLIKYASESISGIPS 80

Qy 61 RFGSGSGTDTLTISLPEPFAVYVYQQSGSWPHTGGTKVEIK 107
Db 81 RFGSGSGTDTLTISRLEPFAFYVYQQSDSWPTTFGQGTKVEIK 127

RESULT 13
US-08-485-246A-10
; Sequence 10, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,246A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6072035ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-246A-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 3.2e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQISGIPA 60
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Qy 61 RFGSGSGTDTLTISLPEPFAVYVYQQSGSWPHTGGTKVEIK 107
Db 81 RFGSGSGTDTLTISRLEPFAFYVYQQSDSWPTTFGQGTKVEIK 127

RESULT 14
US-08-476-176B-6
; Sequence 6, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-176B-6

Query Match 85.1%; Score 474; DB 2; Length 127;
Best Local Similarity 83.2%; Pred. No. 1.2e-37;
Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSIHNLHWYQORPGQAPRLLIYRSQISGIPA 60
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 QY 61 RFSGSGGTDFTLTISLSEPEPFVYVYCOQSGSWPHTFGGKTVEIK 107
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RESULT 15

US-08-127-721A-6
 ; Sequence 6, Application US/08127721A
 ; Patent No. 6066718
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardman, No. 6066718man
 ; APPLICANT: Kolbinger, Frank
 ; APPLICANT: Saldanha, Jose
 ; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
 ; TITLE OF INVENTION: immunoglobulin isotype
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6066718artis Patent and Trademark Department
 ; STREET: 59 Route 10
 ; CITY: East Hanover
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07936-1080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/127,721A
 ; FILING DATE: 27-SEPTEMBER-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/952,802
 ; FILING DATE: 25-SEPTEMBER-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6066718ak, Henry P.
 ; REGISTRATION NUMBER: 33,200
 ; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 277-5110
 ; TELEFAX: (908) 277-4306
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-127-721A-6

Query Match 85.1%; Score 474; DB 3; Length 127;
 Best Local Similarity 83.2%; Pred. No. 1.2e-37;
 Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSIHNLHWYQORPGQAPRLLIYRSQISGIPA 60
 Db 21 DILLTQSPGTLSPGERATLSCRASQISGITHHWYQORPGQAPRLLIYRSQISGIPS 80
 QY 61 RFSGSGGTDFTLTISLSEPEPFVYVYCOQSGSWPHTFGGKTVEIK 107
 Db 81 RFSGSGGTDFTLTISLSEPEPFVYVYCOQSGSWPHTFGGKTVEIK 127

Search completed: October 11, 2001, 12:01:06
 Job time: 916 sec

150 160 170

TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/790,540A

FILING DATE: 30-JAN-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2405

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Initial Score = 9 Optimized Score = 30 Significance = -0.71
Residue Identity = 29% Matches = 35 Mismatches = 70
Gaps = 12 Conservative Substitutions = 0

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70 80 90 100 X

10	220	230	240	250	260	270
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ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Initial Score	=	9	Optimized Score	=	31	Significance	=	-0.70
Residue Identity	=	30%	Matches	=	36	Mismatches	=	69
Gaps	=	12	Conservative Substitutions	=	0			

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:23:38 ; Search time 2122.65 Seconds
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2557.737 Million cell updates/sec

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Perfect score: 351
Sequence: 1 CAGGTGCAGCTGGTGGAGTC.....CTACAGTGACTCTTTCTACT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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96:	gb_in4:*
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98:	em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	268.6	76.5	488	95 S45356	S45356 immunoglobu
5	259.6	74.0	723	10 E21535	E21535 Process for
6	259.6	74.0	761	10 E21533	E21533 Process for
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8	257.4	73.3	413	9 A38870	A38870 Sequence 24

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15 254.8 72.6 351 94 MUSIGHACV
16 254.4 72.5 414 94 MMU62048
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18 254 72.4 354 94 AF113107
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0078815.
ACCESSION AX060780
VERSION AX060780.1 GI:12406160
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 351)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e-104;
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LOCUS AX060784
DEFINITION Sequence 5 from Patent WO0078815.
ACCESSION AX060784
VERSION AX060784.1 GI:12406164
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 351)
JOURNAL Huse, W.D. and Wu, H.
Patent: WO 0078815-A 5 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
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Best Local Similarity 91.9%; Pred. No. 1.7e-88;
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RESULT 3
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LOCUS I08289 482 bp PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0380068.
ACCESSION I08289
VERSION I08289.1 GI:589001
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 482)
AUTHORS Zerler,B.D.
TITLE An expression system for production of chimeric monoclonal antibodies
JOURNAL Patent: EP 0380068-A1 6 01-AUG-1990;
FEATURES Location/Qualifiers
source 1..482
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ORIGIN

Query Match 76.5%; Score 268.6; DB 10; Length 482;
Best Local Similarity 85.9%; Pred. No. 2e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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RESULT 4
S45356

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DEFINITION Partial, 488 nt].
ACCESSION S45356
VERSION S45356.1 GI:255660
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 488)
AUTHORS Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J., Shedd,D., Cahill,K. and Zerler,B.
TITLE Differential effects of a murine and chimeric mouse/human anti-interleukin-2 receptor antibody on human T-cell proliferation
JOURNAL Immunology 76 (3), 452-459 (1992)
MEDLINE 92406249
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibsseq 115041] from the original journal article.
This sequence comes from Fig. 1b.

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BASE COUNT 114 a 116 c 132 g 126 t
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Query Match 76.5%; Score 268.6; DB 95; Length 488;
Best Local Similarity 85.9%; Pred. No. 2e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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RESULT 5
E21535

LOCUS E21535 723 bp DNA PAT 07-FEB-2001
 DEFINITION Process for producing antibody Fas fragment with yeast.
 ACCESSION E21535
 VERSION E21535.1 GI:13023615
 KEYWORDS JP 1999000174-A/4.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS Kyoko,T.T.Y.Y. and Takai,T.T.
 TITLE Process for producing antibody Fas fragment with yeast
 JOURNAL Patent: JP 1999000174-A 4 06-JAN-1999;
 ASahi BREWERIES LTD,THE NIKKA WHISKY DISTILLING CO LTD, TORII
 PHARMACEUT CO LTD,TOMOYASU RI
 COMMENT OS Homo sapiens (human)
 PN JP 1999000174-A/4
 PD 06-JAN-1999
 PF 13-JUN-1997 JP 1997171232
 PR KYOKO TAKAHASHI,TOSHIFUMI YUKI,TOSHIRO TAKAI,TOMOYASU TSURA PC
 C12N15/09,C07K16/28,C12N1/19,C12P21/02,((C12N15/09,C12R1:91), PC
 (C12N1/19,C12R1:84),(C12P21/02,C12R1:84),C12N15/00,(C12N15/00, PC
 C12R1:91)
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT sig peptide 34..99
 FT mat peptide 100..759
 FT mat peptide 763..768.
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 QY 182 TAGACACTGTGAGGCGGCAATTCACCATCTCCAGAGACAATAGTAGACACCCCTATACC 241
 DB 281 CAGACACTGTAAAGGGCCGATTCACCATCTCCAGAGACAATAGTAGACACCCCTATACC 340
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 DB 341 TCGAATGAACAGCTGTGAGAGCGGAGACACAGCCGCTGTATTACTGTGCAAGACATAAT 400
 QY 302 ACGGCAAGTCTGCTGAGAGCGGAGACACAGCCGCTGTATTACTGTGCAAGACATAACT 347
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 E21533
 LOCUS E21533 761 bp DNA PAT 07-FEB-2001
 DEFINITION Process for producing antibody Fas fragment with yeast.
 ACCESSION E21533
 VERSION E21533.1 GI:13023613

KEYWORDS JP 1999000174-A/2.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 761)
 AUTHORS Kyoko,T.T.Y.Y. and Takai,T.T.
 TITLE Process for producing antibody Fas fragment with yeast
 JOURNAL Patent: JP 1999000174-A 2 06-JAN-1999;
 ASahi BREWERIES LTD,THE NIKKA WHISKY DISTILLING CO LTD, TORII
 PHARMACEUT CO LTD,TOMOYASU RI
 COMMENT OS Homo sapiens (human)
 PN JP 1999000174-A/2
 PD 06-JAN-1999
 PF 13-JUN-1997 JP 1997171232
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 (C12N1/19,C12R1:84),(C12P21/02,C12R1:84),C12N15/00,(C12N15/00, PC
 C12R1:91)
 CC Strandedness: Double;
 CC Topology: Linear;
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 FT mat peptide 91..750
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 Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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 DB 152 CTTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 211
 QY 122 CGGGCAAGGGCTGGAGTGGGTGGCCCTTCATTAGTAATCGTGTGTAGCACTACTATT 181
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 QY 182 TAGACACTGTGAGGCGGCAATTCACCATCTCCAGAGACAATAGTAGACACCCCTATACC 241
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 QY 242 TCGAATGAACCTCTGAGAGCGGAGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
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 QY 302 ACGGCAAGTCTGCTGAGAGCGGAGACACAGCCGCTGTATTACTGTGCAAGACATAACT 347
 DB 392 ATGGAGGAATGGACTACTGGGGCAAGGACACCGGTACCGCTC 437
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 DEFINITION Mouse monoclonal antiidiotypic antibody Igm VDJ-region mRNA.
 ACCESSION M83724
 VERSION M83724.1 GI:197951
 KEYWORDS D-region; Ig heavy chain; J-region; V-region; immunoglobulin;
 immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
 SOURCE house mouse.
 ORGANISM Mus musculus

Query Match 73.3%; Score 257.4; DB 9; Length 413;
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Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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DB 244 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAATAGTAGACACACCTTATACC 303

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DB 304 TGCAAATGAGCACTCTGAGAGCTGTGAGAGACAGCCCTGTATTACTGTGCAAGACTACGG 363

QY 302 ACGGCAAGTTTGTCTTACTGGGGCAAGGACTACAGTACTGTTTCT 348
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RESULT 10
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DEFINITION Sequence 15 from patent US 5856456.
ACCESSION AR027762
VERSION AR027762.1 GI:5938582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS Whitlow,M.D. and Filpula,D.R.
TITLE Linker for linked fusion polypeptides
JOURNAL Patent: US 5856456-A 15 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..721
BASE COUNT 176 a 172 c 189 g 184 t
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Best Local Similarity 83.9%; Pred. No. 1e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 62 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121
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QY 242 TGCAAATGAACCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
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QY 302 ACGGCAAGTTTGTCTTACTGGGGCAAGGACTACAGTACTGTTTCT 348
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RESULT 11
AR088763
LOCUS AR088763 721 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 15 from patent US 5990275.
ACCESSION AR088763
VERSION AR088763.1 GI:10015526
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS Whitlow,M.D. and Filpula,D.R.
TITLE Linker and linked fusion polypeptides
JOURNAL Patent: US 5990275-A 15 23-NOV-1999;
FEATURES Location/Qualifiers
source 1..721
BASE COUNT 176 a 172 c 189 g 184 t
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Query Match 73.3%; Score 257.4; DB 9; Length 721;
Best Local Similarity 83.9%; Pred. No. 1e-73; Mismatches 56; Indels 0; Gaps 0;

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QY 62 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121
DB 425 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 484

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QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACAATAGTAGACACACCTTATACC 241
DB 545 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAATAGTAGACACACCTTATACC 604

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QY 302 ACGGCAAGTTTGTCTTACTGGGGCAAGGACTACAGTACTGTTTCT 348
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DEFINITION Sequence 17 from patent US 5856456.
ACCESSION AR027763
VERSION AR027763.1 GI:5938583
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 733)
AUTHORS Whitlow,M.D. and Filpula,D.R.
TITLE Linker for linked fusion polypeptides
JOURNAL Patent: US 5856456-A 17 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..733
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Db 557 TAGACAGTGTGAAGGGCCGATTACCATCTCCAGAGACAGTGCCAGGAACACCCATACC 616

MUSIGHACV

LOCUS MUSIGHACV 351 bp mRNA ROD 27-APR-1993
DEFINITION Mouse Ig H-chain mRNA VDJ-region, partial cds.
ACCESSION M34737
VERSION M34737.1 GI:194750
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain BALB/c) adult spleen anti-HA hybridoma H35-D1, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 351)
AUTHORS Clarke,S.H., Staudt,L.M., Kavaler,J., Schwartz,D., Gerhard,W.U. and Weigert,M.G.
TITLE V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin
JOURNAL J. Immunol. 144, 2795-2801 (1990)
MEDLINE 90203619
FEATURES
Location/Qualifiers
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Search completed: October 11, 2001, 15:09:29
Job time: 6351 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:01:43 ; Search time 2341.88 Seconds
(without alignments)
1416.790 Million cell updates/sec

Title: US-08-791-391A-1

Perfect score: 351

Sequence: 1 CAGGTGCAGTGGTGGAGTC.....CTACAGTGACTGTTTCTAGT 351

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found at <http://www.ncbi.nlm.nih.gov/Genbank/MGC/>

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http://image.llnl.gov
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High quality sequence stop: 649.
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BASE COUNT
ORIGIN
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DEFINITION	601781893F1 NCI_CGAP_Lu30	Mus musculus	cDNA clone	IMAGE:4009847 5', mRNA sequence.
ACCESSION	BF138708			
VERSION	BF138708.1	GI:10977748		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
JOURNAL	1 (bases 1 to 1559)			
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov Tissue procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM9246 row: j column: 24 High quality sequence stop: 562. Location/Qualifiers 1. .1559 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:4009847" /clone_lib="NCI_CGAP_Lu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NOTI; Site 2: Salt; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"			
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	Matches 285;	Conservative 0;	Mismatches 62;	Indels 9;	Gaps 1;
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Db	110	AAGTGAAGATGGTGGAGTCTGGGGGAGGCGCTTAGTGAAGCTGGAGGCTCCCTGAAACTCT	169		
QY	62	CTGTGCAGCCTCTGGANTTCAACCTTCAGTAGCTTATGACATGTTCTTGGGTTCGCAGGCTC	121		
Db	170	CTGTACAGCCTCTGGANTTACCTTCAGTAGTTATGACATGTTCTTGGGTTCGCAGACTC	229		
QY	122	CGGCAAGAGGCTCTGGAGTGGGTGCGCAAAAGCTTAGTAGTGGTGGTGTAGCACCTACTATT	181		
Db	230	CGAGAGAGAGGCTGGAGTGGGTGCGAACCAATTAGTGGTGGTAGTTATACCTACTATC	289		
QY	182	TAGACACTGTGCAGGGCCGATTCCACCATCTCCAGAGACAATAGTAAAGAACCCCTATACC	241		
Db	290	CAGACAGTGTGAAGGGGCGATTCCACCATCTCCAGAGACAATGCCAAGACACCCCTGTTCC	349		

QY	122	CGGCAAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGTGGTGTAGCACCCTACTATT	181
Db	233	CAGAGAAGGGCTGGAGTGGGTTGTCATACATTAGTAGTGCAGTAGTACCATCTACTATG	292
QY	182	TAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC	241
Db	293	CAGACACAGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTGTCC	352
QY	242	TGCAATGAACCTCTCGAGAGCCGAGGACACAGCCGCTGATTACTGTGCAAGAC	298
Db	353	TGCAATGACCAGTCTGAGTCTGAGGACACGCCCATGTATTACTGTGCAAGCCGGGG	412
QY	299	ACTAGGCGAGTTTGTCTACTGGGCCAAGGACTACAGTGA	340
Db	413	GTTCCTCTGTGTTGCTTACCTGGGCCAAGGACTCTGGTCA	454
RESULT 13			
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LOCUS	601786493F1	NCI_CGAP_Lu30 Mus musculus cDNA clone	EST 24-OCT-2000
DEFINITION	mRNA sequence.		
ACCESSION	BF143948		
VERSION	BF143948.1	GI:10982988	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue procurement: Gilbert Smith, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9258 row: i column: 23 High quality sequence stop: 671.		
FEATURES	Location/Qualifiers		
source	1. 862 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:4014430" /clone_lib="NCI_CGAP_Lu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NOTI; Site_2: Salt; transgenic model WNT-1, expression driven by MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	213 a	236 c	236 g 176 t 1 others
ORIGIN			
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Best Local Similarity	80.4%;	Pred. No. 1.6e-58;	
Matches 279;	Conservative	0;	Mismatches 67; Indels 1; Gaps 1;
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Db	100	AGGTGCAGCTGGTGGAGTCTGGGGAGCGCTTAGTGAAGCTTGGAGGTCCCGGAACTCT	159
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Db 160 CCTGTGCAGCCTCTGGATTACATTTTCAGTACTATGGAATGCATCGGTTGGTCAGGCTC 219
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Db 220 CAGAGAGGGCTGGAGTGGTTCATACATTAGTACTGGCAGTAGTACCATCTACTATG 279
QY 182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAACAACCCCTATACC 241
Db 280 CAGACACAGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCTGTTC 339
QY 242 TGCATAATGAATCTCTCAGAGCCGAGCAGACAGCCGCTGTTACTGTGCAAGACATACT 301
Db 340 TGCATAATGACAGCTTAAGTCTGAGACACAGCCGCTGTTACTGTGCAAGGCCAGGTT 399
QY 302 ACAGCAGCT-TTTGGTACTGGGGCAAGGAGGACTACAGTACTGTTTC 347
Db 400 ACTCCCTATCGGACTACTGGGTCAAGGACCTCAGTACCCTGCTC 446

RESULT 14
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LOCUS UI-HF-BK0-abj-e-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056371 5', mRNA sequence.
ACCESSION AW408304
VERSION AW408304.1 GI:6927361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 440)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3056371"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonatido, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 99 a 98 c 134 g 109 t
ORIGIN
Query Match 64.6%; Score 226.8; DB 115; Length 440;
Best Local Similarity 82.1%; Pred. No. 2.7e-58; Indels 0; Gaps 0;
Matches 261; Conservative 0; Mismatches 57;

QY 2 AGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCGCTGGAAGCTCCTGAGACTCT 61
Db 120 AGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCGCTGGAAGCTCCTGAGACTCT 179

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QY 62 CCTGTGCAGCCTCTGGATTACATTTTCAGTACTATGACATGTCTTTGGTTGGCCAGGCTC 121
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QY 122 CGGCAAGGGTCTGGAGTTCGCAAAAGTTAGTACTGGTGGTGGTAGCACCTACTATT 181
Db 240 CAGGAAAGGGCTGGAGTGGTTCATACATTAGTACTGGTGGTAGTACCATATACAG 299
QY 182 TAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATAGTAAACAACCCCTATACC 241
Db 300 CAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAAGCCCAAGACTCACTGTATC 359
QY 242 TGCATAATGAATCTCTCAGAGCCGAGCAGACAGCCGCTGTTACTGTGCAAGACATACT 301
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QY 302 ACAGCAGTCTTGGTACT 319
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RESULT 15
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DEFINITION mRNA sequence.
ACCESSION BF136279
VERSION BF136279.1 GI:10975319
KEYWORDS Est.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 718)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLaM9244 row: 0 column: 22
High quality sequence stop: 671.
FEATURES
Location/Qualifiers
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/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPO6T6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 173 a 196 c 181 g 168 t
ORIGIN
Query Match 64.6%; Score 226.8; DB 145; Length 718;
Best Local Similarity 80.3%; Pred. No. 3.1e-58;
Matches 278; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

QY 2 AGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCGCTGGAAGCTCCTGAGACTCT 61
Db 102 AGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCGCTGGAAGCTCCTGAGACTCT 161

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Job time: 5536 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:24:48 ; Search time 177.65 Seconds
(without alignments)
1240.605 Million cell updates/sec

Title: US-08-791-391A-1

Perfect score: 351

Sequence: 1 CAGGTGACGTGTGGAGTC.....CTACAGTGAAGTCTTCTAGT 351

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	100.0	351	19 AAV49820	Vitaxin antibody h
2	351	100.0	351	22 AAF28175	Vitaxin heavy chain
3	302.2	86.1	351	19 AAV49822	LM609 antibody hea
4	302.2	86.1	351	22 AAF28177	Antibody LM609 hea
5	268.6	76.5	482	11 AAQ05555	Sequence encoding
6	263.8	75.2	417	15 AAQ02804	Humanised murine K
7	263.8	75.2	417	16 AAQ07534	Humanised anti-KC-
8	259.6	74.0	582	18 AAT90020	DNA encoding heavy
9	259.6	74.0	761	20 AAX01214	Human antiFc epsil
10	259.6	74.0	770	20 AAX01216	Human antiFc epsil
11	257.4	73.3	413	15 AAQ68650	MAB A33 heavy chain

12	257.4	73.3	721	20 AAV99765	A33/212 single-cha
13	257.4	73.3	721	21 AAZ37397	Linked fusion prot
14	257.4	73.3	733	20 AAV99766	A33/218 single-cha
15	257.4	73.3	733	21 AAZ37398	Linked fusion prot
16	255	72.6	1938	19 AAV58929	A33 chimeric recep
17	252.4	71.9	411	19 AAV24243	Chimeric antibody
18	252.4	71.9	411	20 AAX00116	Human antibody hea
19	252.4	71.9	411	21 AAZ58914	DNA seq ID No: 58
20	252.4	71.9	411	22 AAF69130	Human antibody H c
21	252.4	71.9	411	22 AAF69186	Human antibody H c
22	252.4	71.9	411	22 AAF63242	Human antibody H c
23	251	71.5	351	16 AAQ96284	Human IgE receptor
24	249.4	71.1	351	16 AAQ96282	Human IgE receptor
25	249.4	71.1	351	18 AAT90025	cDNA encoding heav
26	249.2	71.0	411	19 AAV24232	Chimeric antibody
27	249.2	71.0	411	20 AAX00092	Mouse humanised an
28	249.2	71.0	411	21 AAZ58913	Mouse antibody H c
29	249.2	71.0	411	22 AAF69129	Human pThrp mouse
30	249.2	71.0	411	22 AAF69185	Human pThrp mouse
31	249.2	71.0	411	22 AAF69241	Human pThrp mouse
32	247.4	70.5	369	19 AAV07642	anti-CD22 monoclon
33	246.8	70.3	1329	18 AAT61281	Humanised anti-L-s
34	246.2	70.1	480	13 AAQ20070	MRK16-H chain. Ch
35	244.8	69.7	418	15 AAQ62764	Murine KC-4 immuno
36	244.8	69.7	418	15 AAQ62789	Murine KC-4 immuno
37	244.4	69.6	722	21 AAZ28996	Anti-human CTLA-4
38	244.4	69.6	729	21 AAZ28997	Anti-murine CTLA-4
39	243.6	69.4	414	21 AAZ35243	Humanised anti-ver
40	242.2	69.0	324	13 AAQ20303	B cell hybridoma l
41	241.4	68.8	357	15 AAQ66409	VH coding region o
42	240.6	68.5	360	19 AAV04636	Chimeric humanised
43	240.6	68.5	720	19 AAV04638	Chimeric humanised
44	240.2	68.4	354	18 AAT43417	Xenograft antibody
45	240	68.4	441	18 AAT72269	Chimeric MAB 15 PC

ALIGNMENTS

RESULT 1

AAV49820
ID AAV49820 standard; DNA; 351 BP.

XX AC AAV49820;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region DNA.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers
XX FT CDS 1..351
XX FT /*tag= a
XX FT /product= "vitaxin antibody heavy chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"

XX WO98333919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX 1..351

XX CDS

XX /*tag= a

XX /product= "LM609 antibody heavy chain variable region"

XX /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

XX LM609, also related nucleic acid, used to treat, prevent or diagnose

XX angiogenesis or restenosis

XX Claim 37; Fig 2a; 129pp; English.

XX This sequence encodes the LM609 antibody variable heavy chain region.

XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3

XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus

XX block integrin-mediated signal transduction. This is useful in the

XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,

XX specifically angiogenesis and restenosis (but also e.g. (non-)immune

XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,

XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

XX etc.). The antibodies contain non-murine framework regions so are

XX suitable for use in humans. Enhanced types of LM609 have affinity more

XX than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

SQ

Query Match 86.1%; Score 302.2; DB 19; Length 351;

Best Local Similarity 91.9%; Pred. No. 1.5e-84;

Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 62 CCTGTGCAGCCTCTGAGTTCACCTTCAGTAGCTATGACATGCTTGGGTCCGCCAGGCTC 121

DB 62 cctgtgcagcctctgagttcgttccagtagctatgacatgcttctgggtccgagattc 121

QY 122 CGGGCAAGGCTGTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181

DB 122 cggagaagagctgtgagtggtggtgcgaaagttagtgagtggtgtagcactatt 181

QY 182 TAGACACTGTGCGAGCGGATTCACATCTCCAGAGACAAATAGTAGAAGACACCCATATAC 241

DB 182 tagacactgtgcagggcgattccacatctccagagacaatgccagaacacccataacc 241

QY 242 TCCAAATGACACTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAACACATACT 301

DB 242 tgcaaatgagcgtctgagcctgaggacacagccgatgtattactgtgcaagacataact 301

QY 302 ACGCAGGTTTCTTACTGGGCGCCAGGACTACAGTGACTCTTTCT 348

DB 302 acggcagtttcttactctggggccaaggagactctggtcactctct 348

RESULT 4

AAF28177

XX AAF28177 standard; DNA; 351 BP.

XX AAF28177;

XX 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region DNA.

XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;

XX inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

XX osteoporosis -

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

XX exhibiting selective binding affinity to alphavbeta_3 integrin or

XX their functional fragments. The antibodies or their functional

XX fragments can be used in the diagnosis and treatment of

XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory

XX diseases (such as psoriasis and chronic articular rheumatism),

XX disorders associated with inappropriate or inopportune invasion of

XX vessels (such as diabetic retinopathy, neovascular glaucoma and

XX cancer disorders such as tumours and Kaposi's sarcoma), retinal

XX diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

SQ

Query Match 86.1%; Score 302.2; DB 22; Length 351;

Best Local Similarity 91.9%; Pred. No. 1.5e-84;

Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGGTGTGTCAGCCTGGAAGTCCCTGAGACTCT 61

DB 2 aagtgcagctgtgagctgtgggaggttagtgagcctggaaggtccctgagactct 61

QY 62 CCTGTGCAGCCTCTGAGTTCACCTTCAGTAGCTATGACATGCTTGGGTCCGCCAGGCTC 121

DB 62 cctgtgcagcctctgagttcgttccagtagctatgacatgcttctgggtccgagattc 121

QY 122 CGGGCAAGGCTGTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181

DB 122 cggagaagagctgtgagtggtggtgcgaaagttagtgagtggtgtagcactatt 181

QY 182 TAGACACTGTGCAGGCGCGATTCCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
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 QY 242 TGCAAATGAACCTCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
 Db 242 tgcaaatgagcagctggaactctgagacacagccatgtattactgtgcaagacataact 301
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 Db 302 acggcagttttgcttactggggccaaggactctgtgcaactgtctct 348
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 AC AAQ05555;
 XX XX
 DT 10-DEC-1990 (first entry)
 XX XX
 DE Sequence encoding variable region of murine AHT 54 heavy chain.
 XX XX
 KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
 XX XX
 OS Mus sp.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 75..482
 FT /*tag= a
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 PN EP380068-A.
 XX XX
 PD 01-AUG-1990.
 XX XX
 PF 24-JAN-1990; 90EP-0101351.
 XX XX
 PR 04-DEC-1989; 89US-0441702.
 PR 24-JAN-1989; 89US-0301216.
 XX XX
 PA (MOLE-) MOLECULAR THERAPEU.
 XX XX
 PI Zerler B;
 XX XX
 DR WPI; 1990-232892/31.
 DR P-PSDB; AAR06251.
 XX XX
 PT Expression vectors for producing chimeric monoclonal antibodies -
 PT which express human constant region and non-human variable region
 XX XX
 PS Disclosure; ; p; English.
 XX XX
 CC MAbs comprising mouse CH and CL constant regions with human
 CC variable regions may be used to create mouse/human hybrid MAbs,
 CC which have a longer serum half-life. Method can be used to produce
 CC Abs against interleukin-2 receptor and tumour necrosis factor.
 XX XX
 SQ Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;
 Query Match 76.5%; Score 268.6; DB 11; Length 482;
 Best Local Similarity 85.9%; Pred. No. 4.6e-74;
 Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 2 AGCTGCAGCTGTGGAGCTGGGGAGGCGCTTGTGCAGCTGGAAGGTCCTGAGACTCT 61
 Db 133 aagtcagctgtg99agctc99ggagccttagtagcagcctgagggctccctgaaactct 192
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 Db 193 cctgtcagcctctggaattcgtcttcagtagcattgacatgtcttggttcgcagactc 252
 QY 122 CGGCGAAGGCTCTGGAGTGGGTGCGAAGTCTAGTAGTGGTGGTAGCACCTACTATT 181

Db 253 cggagaagagcgtggagtggtcgcatatacatattagtagtggtgataacacactactatc 312
 QY 182 TAGACACTGTGCAGGCGCGATTCCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
 Db 313 cagacactgtgaagggccgattccaccatctccagagacaatgccaagaacaccccttacc 372
 QY 242 TGCAAATGAACCTCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
 Db 373 tgcaaatgagcagctctgaaagtctgagagacacagccgtgtattactgtgcaagaaggtacg 432
 QY 302 ACGGCAGTTTTGCTTACTGGGGCCAAAGGGACTACAGTGACTGTTTCT 348
 Db 433 gcctcccttttgccttactggggccaaggactctgtgcaactgtctct 479
 RESULT 6
 AAQ62804
 ID AAQ62804 standard; DNA; 417 BP.
 AC AAQ62804;
 XX XX
 DT 25-JAN-1995 (first entry)
 XX XX
 DE Humanised murine KC-4 immunoglobulin heavy chain V-region DNA.
 XX XX
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human mammary fat globule; human breast carcinoma;
 KW murine anti-HMPG monoclonal antibody KC-4; humanised analogue; ss.
 XX XX
 OS Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 1..416
 FT /*tag= a
 FT /*note= "humanised KC-4 VH chain"
 FT mat_peptide 58..416
 FT /*tag= b
 FT /*product= heavy_chain_V-region
 FT /*note= "humanised framework region"
 XX XX
 PN W09411509-A.
 XX XX
 PD 26-MAY-1994.
 XX XX
 PF 16-NOV-1993; 93WO-US11445.
 XX XX
 PR 16-NOV-1992; 92US-0977696.
 PR 30-SEP-1993; 93US-0129930.
 PR 08-OCT-1993; 93US-0134346.
 XX XX
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 XX XX
 PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
 XX XX
 DR WPI; 1994-183510/22.
 DR P-PSDB; AAR52823.
 XX XX
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms
 XX XX
 PS Example 67; Page 91; 109pp; English.
 XX XX
 CC This DNA sequence encodes a humanised murine anti-human carcinoma
 CC antibody heavy chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.
 XX XX
 SQ Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;


```
PT antigenicity in humans
PS Disclosure; Fig 9; 26pp; Japanese.
XX
CC The present sequence, which encodes the heavy chain variable
CC region of the human antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAB), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAb. The humanised,
CC semi-chimeric or chimeric MAB can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
XX
SQ Sequence 582 BP; 133 A; 134 C; 155 G; 160 T; 0 other;

Query Match 74.0%; Score 259.6; DB 18; Length 582;
Best Local Similarity 84.4%; Pred. No. 3.1e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGCTGTGGGGAGCGCTGTGCGAGCCTGGAAGCTCCCTGAGACTCT 61
DB 220 aggtgcagctgtgtgagctgtggggagcgctgtgcccagcctgggggtccctgagactct 279
QY 62 CCTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 121
DB 280 cctgtgcagcctctggattcaccttttagtacctatccattgtcttgggtccgcagctc 339
QY 122 CGGCGAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGTGGTGGTAGCACCTACTATT 181
DB 340 cagggaagggtctggagtggtggtccttattagtaacgtggtgtagcacctactatc 399
QY 182 TAGACACTGTGCAGCGCGGATTTCACCTCTCCAGAGCAATAGTAAGAACACCCCTATACC 241
DB 400 cagacactgtaaaggccgattccacctccagagacaacccaagaactcactgtatc 459
QY 242 TGCAAAATGAACCTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 460 tgcaaatgaacagctgtagagccgagagacacggtgtgtattactgtgcgagacataatt 519
QY 302 ACGCAGTGTGTGCTTACTTGGGGCCAAAGGACTACAGTGACTGTTC 347
DB 520 atggaggaatggactacttggggccaaaggaccacggtcacgcgtctc 565

RESULT 9
AAX01214
ID AAX01214 standard; cDNA to mRNA; 761 BP.
XX
AC AAX01214;
XX
XX 31-MAR-1999 (first entry)
XX
DE Human antiFc epsilon RI alpha chain antibody coding sequence #2.
XX
KW AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..753
FT /*tag= a
FT sig_peptide 34..90
FT /*tag= b
FT mat_peptide 91..750
FT /*tag= c
XX
XX JF11000174-A.
XX
XX 06-JAN-1999.
XX
XX ,13-JUN-1997; 97JP-0171232.
XX
```

```
PR 13-JUN-1997; 97JP-0171232.
XX
XX (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIH KK.
XX (TSUR/) TSURA T.
XX
XX WPI; 1999-124394/11.
DR P-PSDB; AAW73874.
XX
XX Preparing an antibody Fab fragment using yeast - in high yield
PT
XX
XX Claim 6; Page 7; 13pp; Japanese.
XX
CC This sequence encodes a human antiFc epsilon RI alpha chain antibody,
CC produced using the method of the invention. The method is for preparing
CC an antibody Fab fragment using the yeast Pichia pastoris as the host
CC cell. The method can prepare an antibody Fab fragment cost efficiently
CC and in high yield.
XX
SQ Sequence 761 BP; 166 A; 228 C; 206 G; 161 T; 0 other;

Query Match 74.0%; Score 259.6; DB 20; Length 761;
Best Local Similarity 84.4%; Pred. No. 3.4e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGCTGTGGGGAGCGCTGTGCGAGCCTGGAAGCTCCCTGAGACTCT 61
DB 92 aggtgcagctgtgtgagctgtggggagcgctgtgcccagcctgggggtccctgagactct 151
QY 62 CCTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 121
DB 152 cctgtgcagcctctggattcaccttttagtacctccattgtcttgggtccgcagctc 211
QY 122 CGGCGAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGTGGTGGTAGCACCTACTATT 181
DB 212 cagggaagggtctggagtggtggtccttattagtaacgtggtgtagcacctactatc 271
QY 182 TAGACACTGTGCAGCGCGGATTTCACCTCTCCAGAGCAATAGTAAGAACACCCCTATACC 241
DB 272 cagacactgtaaaggccgattccacctccagagacaacccaagaactcactgtatc 331
QY 242 TGCAAAATGAACCTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 332 tgcaaatgaacagctgtagagccgagagacacggtgtgtattactgtgcgagacataatt 391
QY 302 ACGCAGTGTGTGCTTACTTGGGGCCAAAGGACTACAGTGACTGTTC 347
DB 392 atggaggaatggactacttggggccaaaggaccacggtcacgcgtctc 437

RESULT 10
AAX01216
ID AAX01216 standard; cDNA to mRNA; 770 BP.
XX
AC AAX01216;
XX
XX 31-MAR-1999 (first entry)
XX
DE Human antiFc epsilon RI alpha chain antibody coding sequence #4.
XX
KW AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 34..762
FT /*tag= a
FT sig_peptide 34..99
FT /*tag= b
FT mat_peptide 100..759
FT /*tag= c
XX
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XX JP11000174-A.
 XX 06-JAN-1999.
 XX 13-JUN-1997; 97JP-0171232.
 XX 13-JUN-1997; 97JP-0171232.
 XX (ASAK) ASahi BREWERIES LTD.
 XX (NIKK-) NIKKA WHISKEY KK.
 XX (TORI) TORII YAKUHIH KK.
 XX (TSUR/) TSURA T.
 XX WPI; 1999-124394/11.
 XX P-PSDB; AAW73876.
 XX Preparing an antibody Fab fragment using yeast - in high yield
 XX Claim 6; Page 9-10; 13pp; Japanese.
 XX This sequence encodes a human antiFc epsilon RI alpha chain antibody,
 CC produced using the method of the invention. The method is for preparing
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host
 CC cell. The method can prepare an antibody Fab fragment cost efficiently
 CC and in high yield.
 XX Sequence 770 BP; 172 A; 223 C; 205 G; 170 T; 0 other;
 SQ

Query Match 74.0%; Score 259.6; DB 20; Length 770;
 Best Local Similarity 84.4%; Pred. No. 3.4e-71;
 Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTCACCTGGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAGAGTCCCTGAGACTCT 61
 Db 101 aggtgcagctggtgagctggtggtggtggtggtggtggtggtggtggtggtggtggt 160

QY 62 CCGTGGCAGCCTCTGAGTTCACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121
 Db 161 cctgtgcagctctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 220

QY 122 CGGCAAGGCTGTGGAGTGGTGGCAAGATTAGTAGTGGTGGTGGTGGTGGTGGTGGTGG 181
 Db 221 cagggaaggctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 280

QY 182 TAGACACTGTGAGCGGCGATTCACCTCTCCAGAGACAATAGTAGAACACCCCTATACC 241
 Db 281 cagacactgtaaaggccgattccacctctccagagacacagccagacacacacacacac 340

QY 242 TGCAATCAACTCTCTGAGAGCGGAGGACACAGAGCGGTGTATTACGTGCAAGACATAACT 301
 Db 341 tgcataatcaactctctgagagcggagacacagagcgggtgtattacgtgcaagacataact 400

QY 302 ACGCGAGTTTGTCTTACTGGGCGCAAGGAGTACAGTGGTGGTGGTGGTGGTGGTGGTGG 347
 Db 401 atggagggaagtactactggtgggcaaggagacacaggtcacggtcacggtcacggtcac 446

RESULT 11
 AAQ68650
 ID AAQ68650 standard; DNA; 413 BP.
 XX
 AC AAQ68650;
 XX
 DT 13-FEB-1995 (first entry)
 XX
 DE MAB A33 heavy chain coding sequence.
 XX
 KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;
 KW heavy; chains; VH; humanised; antibody; vectors; expression; human;
 KW secretion; A33; Fab (gamma/delta/cys); pcg16; ompa signal; C-kappa;
 KW pskomp; pmRR055; CH1 domains; hinge; deltaCys; pmRR022; pmRR109;

antigen; diagnosis; treatment; colorectal cancer; metastases; ss.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT primer_bind 1..32 /*tag= a
 FT CDS 6..413 /*tag= b
 FT sig_peptide 6..62 /*tag= c
 FT mat_peptide 63..413 /*tag= d
 FT primer_bind 396..413 /*tag= e
 XX
 PN W09413805-A.
 XX
 PD 23-JUN-1994.
 XX
 PF 10-DEC-1993; 93WO-GB02529.
 XX
 PR 10-DEC-1992; 92GB-0025853.
 PR 22-JUL-1993; 93GB-0015249.
 XX
 PA (CLLT) CELLTech LTD.
 XX
 PI Adair JR, King DJ, Owens RJ;
 XX
 DR WPI; 1994-217881/26.
 DR P-PSDB; AAR56962.
 XX
 PT Humanised antibodies raised against A33 antigen - are used for
 PT diagnosis or treatment of colorectal tumours and metastases
 XX
 PS Example 1; Fig 3(11); 90pp; English.
 XX
 CC The sequences given in AAQ68649-50 encode the light and heavy chain
 CC variable regions (VH and VL) of the humanised anti-A33 antibody of
 CC the invention. These fragments were produced by PCR using the primer
 CC sequences given in AAQ68624-48. The amplified fragments were used in
 CC the construction of vectors for the expression and secretion of the
 CC chimeric humanised A33. The amplified products were cleaved with BstBI
 CC and SphI for the light chain and HindIII and ApaI for the heavy chain.
 CC These fragments were cloned into the human kappa light chain acceptor
 CC vector, pmRR15.1, and the human heavy chain, IgG1, acceptor vector,
 CC pmRR011 respectively, to give chimeric expression vector PRO108 for the
 CC light chain and PRO107 for the heavy chain. Proteins which bind the A33
 CC antigen can be used in the diagnosis or treatment of colorectal cancers
 CC and metastases.
 XX
 SQ Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;
 XX

Query Match 73.3%; Score 257.4; DB 15; Length 413;
 Best Local Similarity 83.9%; Pred. No. 1.3e-70;
 Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAGGTCCTGGAGACTCT 61
 Db 64 aagtgaagctggtgagctgctgggaggttagtgaagctgaggtggtcctgaaactct 123

QY 62 CCGTGGCAGCCTCTGAGTTCACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121
 Db 124 cctgtgcagcctctggttgcagtcacatgacatgcttgcgttgcgttgcgttgcgttgc 183

QY 122 CGGCAAGGCTGTGGAGTGGTGGCAAGATTAGTAGTGGTGGTGGTGGTGGTGGTGGTGG 181
 Db 184 cggagaagagctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 243

QY 182 TAGACACTGTGAGCGGCGGATTCACCTCTCCAGAGACAATAGTAGAACACCCCTATACC 241
 Db 241 tgcataatcaactctctgagagcggagacacagagcgggtgtattacgtgcaagacataact 301

Db 244 tagacagtgtgaagggccgattaccatctccagagacagtgcaggaaacacctatacc 303
 QY 242 TGCAAAATGAATCTCTCAGAGCCGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
 Db 304 tgcgaatgagacgtctgaggtctgagagacacgctctgtattactgtgcaccgactacg 363
 QY 302 ACGGCAGATTTTGTCTACTGTGGGCCAAGGGACTACAGTGAAGTCTTCT 348
 Db 364 tagtcccgcttctactgggccaaggagactctgtgtcaccgtctct 410

RESULT 12

AAV99765
 ID AAV99765 standard; DNA; 721 BP.

AC AAV99765;
 XX

DT 23-MAR-1999 (first entry)

XX A33/212 single-chain Fv coding sequence.

XX Linker: fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
 KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;
 KW aggregation; ds.

XX Synthetic.

XX Key Location/Qualifiers

FH 1..711

FT CDS

FT /tag- a

FT /product= "A33/212 scFv"

FT /note= "The start codon is not indicated"

FT misc_feature 1..321

FT /tag- b

FT /note= "sequence coding for A33 V1 region"

FT misc_feature 322..363

FT /tag- c

FT /note= "sequence coding for peptide linker 212"

FT misc_feature 364..708

FT /tag- d

FT /note= "sequence coding for A33 Vh region"

XX US5856456-A.

XX 05-JAN-1999.

XX PF 07-APR-1994; 94US-0224591.

XX PR 07-APR-1994; 94US-0224591.

XX PR 20-NOV-1992; 92US-0980529.

XX PR 15-JAN-1993; 93US-0002845.

XX (ENZO-) ENZON INC.

XX PI Filpula DR, Whitlow MD;

XX WPI; 1999-105193/09.

XX P-PSDB; AAW95440.

XX DNA encoding fusion polypeptide including protease resistant linker

XX - for making single-chain Fv antibody fragments, e.g for diagnosis

XX and treatment of cancer

XX Disclosure; Fig 12; 39pp; English.

XX The invention is directed to a novel peptide linker useful for connecting

XX polypeptide constituents into a novel linked fusion polypeptide. The

XX peptide linker includes at least one XP motif (where X is a charged

XX amino acid) and includes any of these sequences (GTSXSGXPGSGSGSTRK;

XX GTSXSGXPGSGSTRK; or GTSXSGXPGK) to inhibit its proteolysis by

XX subtilisin or trypsin. DNA molecules encoding fusion polypeptides

XX containing two polypeptides, derived from the same multichain protein of

XX the immunoglobulin (Ig) superfamily and a peptide linker as above, are

CC particularly used to prepare single chain antibody Fv fragments (scFv),
 CC potentially useful for diagnosis and treatment of cancer. The fusion
 CC polypeptide containing the specified linkers is proteolytically stable
 CC (associated with positioning of the P residue) and resistant to
 CC aggregation, while residue X improves solubility. The present sequence
 CC represents the nucleotide sequence of a A33/212 scFv fragment.
 XX
 SQ Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

Query Match 73.3%; Score 257.4; DB 20; Length 721;

Best Local Similarity 83.9%; Pred. No. 1.6e-70;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGGAGGCGTGTGTGAGCCTGGAAGTCCCTCAGACTCT 61

Db 365 aagtgaagctgtggaagctgtggaagctgtggaagctgtggaagctgtggaagctgt 424

QY 62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121

Db 425 cctgtgcagcctctggaattcgtttcagtaacctatgacatgtcttgggttcgcagactc 484

QY 122 CGGGCAAGGGTCTGGAGTGGTGGCAAAAGTTAGTAGTGTGTGTGTGTGTGTGTGT 181

Db 485 cggagaagagggctggagtggtggtgcgaacctattagtagtggtggtggtggtggt 544

QY 182 TAGACACTGTGCAGGGCCGATTCCACCATCTCCAGAGACATAAGTAAAGACACCTATACC 241

Db 545 tagacagtgtgaagggccgattccacctctccagagacagtgccaggaacacctatacc 604

QY 242 TGAATATGAATCTCTGAGAGCCGAGGACACACCGCTGTATTACTGTGCAAGACATAACT 301

Db 605 tgcgaatgagcagctgaggtctgaggtgaggtgaggtgaggtgaggtgaggtgaggt 664

QY 302 ACGGCAGATTTTGTCTACTGTGGGCCAAGGGACTACAGTGAAGTCTTCT 348

Db 665 tagtcccgcttctactgggccaaggagactctgtgtcaccgtctct 711

RESULT 13

AAZ37397

ID AAZ37397 standard; DNA; 721 BP.

XX AC AAZ37397;

XX DT 08-FEB-2000 (first entry)

XX DE Linked fusion protein A33/212 sfv coding sequence.

XX Fv fusion protein; linker; linked fusion polypeptide; multichain protein;

XX protein complex; antibody; ss.

XX OS Synthetic.

XX PN US5990275-A.

XX PD 23-NOV-1999.

XX PF 10-SEP-1997; 97US-0926789.

XX PR 07-APR-1994; 94US-0224591.

XX PR 20-NOV-1992; 92US-0980529.

XX PR 15-JAN-1993; 93US-0002845.

XX (ENZO-) ENZON INC.

XX PI Filpula DR, Whitlow MD;

XX WPI; 2000-022812/02.

XX Peptide linkers, linked fusion polypeptides containing the linkers and

XX their preparation -

XX

Db 677 tagtcccgtttgccttactggggccaaagggaactctgtgtaactgtctct 723

Search completed: October 11, 2001, 15:12:35
Job time: 6467 sec

ID AAZ37398 standard; DNA; 733 BP.
XX AAZ37398;
XX
XX
DT 08-FEB-2000 (first entry)
XX
XX Linked fusion protein A33/218 sfv coding sequence.
DE
XX
KW Fusion protein; linker; linked fusion polypeptide; multichain protein;
KW protein complex; antibody; ss.
XX
XX Synthetic.
XX
XX US5990275-A.
XX
XX 23-NOV-1999.
XX
XX
XX 10-SEP-1997; 97US-0926789.
XX
XX
XX 07-APR-1994; 94US-0224591.
XX
XX 20-NOV-1992; 92US-0980529.
XX
XX 15-JAN-1993; 93US-0002845.
XX
XX (ENZO-) ENZON INC.
XX
XX
XX Filpula DR, Whitlow MD;
XX
XX
XX WPI; 2000-022812/02.
XX
XX P-PSDB; AAY54837.
XX
XX
XX Peptide linkers, linked fusion polypeptides containing the linkers and
XX their preparation -
XX
XX
XX Example; Fig 13; 42pp; English.

XX This sequence encodes a linked fusion protein containing the
XX amino acid linker of the invention. The linkers are used for connecting
XX constituent polypeptides to form novel linked fusion polypeptides.
XX Polypeptides derived from any protein can be connected, in particular
XX multichain protein or protein complexes e.g. enzymes, members of the
XX immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
XX provides fusion proteins which have greater stability and are less
XX susceptible to aggregation.
XX
XX Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 21; Length 733;
Best Local Similarity 83.9%; Pred. No. 1.6e-70;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGTCCCTGAGACTCT 61
DB 377 aagtgaagcttggagtgctggggaggttagtgagcctgaggggtccctgaaactct 436
QY 62 CCTGTGCAGCCTCTGATTCACCTCTCAGTAGCTATGACATGCTTGGGTGCCAGGCTC 121
DB 437 cctgtgcagcctctggagctcgttcagctacatgacatgcttgggtgcgcagactc 496
QY 122 CGGCGAAGGCTGTGGAGTGGTGGCAAAAGTTAGTAGTGTGTGTAGCACCTACTATT 181
DB 497 cggagaagaggctggagtggtggcgaaccattagtagtggtgtagttacacctactatt 556
QY 182 TAGACACTGTGACGGCCGATTACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241
DB 557 tagacagtgtgaaggccgattccaccatctccagagacagtgcaggaacacccataacc 616
QY 242 TGCAAATGACTCTCTGAGNGCCGAGACACAGCCGTGTATTACTGTGCAAGACATACT 301
DB 617 tgcgaatgacagtctgaggtctgagacacagcgcctgtattactgtgacccgactacgg 676
QY 302 ACGGCAGTTTGTCTTACTGTTGGGCAAGGACTACAGTGACTGTCTTCT 348

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:50:53 ; Search time 87.94 Seconds
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Title: US-08-791-391a-1
Perfect score: 351
Sequence: 1 CAGGTGACGTGCTGGAGTC.....CTACAGTGACTGTTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	257.4	73.3	413	1	US-08-253-877C-56
2	257.4	73.3	413	2	US-08-452-164A-56
3	257.4	73.3	721	2	US-08-224-591-15
4	257.4	73.3	721	2	US-08-926-789-15
5	257.4	73.3	733	2	US-08-224-591-17
6	257.4	73.3	733	2	US-08-926-789-17
7	246.8	70.3	405	4	US-08-579-378A-19
8	246.8	70.3	1329	5	PCT-US96-13152-3
9	244.8	69.7	418	1	US-07-977-696C-27
10	244.8	69.7	418	1	US-08-129-930B-27
11	240.6	68.5	360	2	US-08-672-176A-5
12	240.6	68.5	720	2	US-08-672-176A-5
13	239.8	68.3	357	1	US-08-475-000-15
14	239.8	68.3	357	2	US-08-483-199-15
15	239.8	68.3	357	2	US-08-484-508-15
16	238.2	67.9	445	1	US-08-053-171-10
17	238.2	67.9	491	1	US-08-053-171-6
18	237.2	67.6	717	2	US-08-553-497A-17
19	236.6	67.4	717	2	US-07-956-399-3
20	235.6	67.1	357	1	US-08-331-398A-21
21	235.6	67.1	357	1	US-08-207-996-26
22	235.6	67.1	357	2	US-08-760-840A-26
23	235.6	67.1	357	2	US-08-760-840A-27
24	235.6	67.1	357	2	US-08-331-397B-21
25	235.6	67.1	357	2	US-08-759-804A-21
26	235.6	67.1	357	3	US-09-266-119-26
c 27	235.6	67.1	357	3	US-09-266-119-27

28	235.6	67.1	375	1	US-08-331-398A-59	Sequence 59, Appl
29	235.6	67.1	375	2	US-08-331-397B-59	Sequence 59, Appl
30	235.6	67.1	375	2	US-08-759-804A-58	Sequence 58, Appl
31	235.6	67.1	738	1	US-08-331-398A-31	Sequence 31, Appl
32	235.6	67.1	738	2	US-08-331-397B-31	Sequence 31, Appl
33	235.6	67.1	738	2	US-08-759-804A-31	Sequence 31, Appl
34	235.4	67.1	923	5	PCT-US94-07659-1	Sequence 1, Appl
35	235	67.0	354	4	US-08-487-761-14	Sequence 14, Appl
36	234.8	66.9	417	1	US-08-398-613A-21	Sequence 21, Appl
37	234.8	66.9	417	1	US-08-398-612A-21	Sequence 21, Appl
38	234.8	66.9	417	1	US-08-398-611A-21	Sequence 21, Appl
39	234.8	66.9	417	1	US-08-396-851A-21	Sequence 21, Appl
40	234.8	66.9	417	2	US-08-491-334A-21	Sequence 21, Appl
41	234.8	66.9	417	3	US-09-027-449-18	Sequence 18, Appl
42	234.8	66.9	417	3	US-08-804-444A-18	Sequence 18, Appl
43	234.8	66.9	417	3	US-09-026-985-18	Sequence 18, Appl
44	234.8	66.9	756	1	US-08-398-613A-29	Sequence 29, Appl
45	234.8	66.9	756	1	US-08-398-612A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-253-877C-56
; Sequence 56, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
US-08-253-877C-56

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Query Match 73.3%; Score 257.4; DB 1; Length 413;
Best Local Similarity 83.9%; Pred. No. 3.7e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGGTGGAGTCTGGGGAGGCGTTGTGACAGCTGGAAGGTCCTGAGACTCT 61
DB 64 AAGTGAAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGAGCTGGAGGTCCTGAAACTCT 123
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGCTC 121
DB 124 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGCTC 183
QY 122 CGGCAAGGCTGGAGTCTGGGAGGCGTTGTGAGTAGTGTGTTAGTACCTACTATT 181
DB 184 CGGAGAGGCTGGAGTCTGGGAGGCGTTGTGAGTAGTGTGTTAGTACCTACTATT 243
QY 182 TAGACACTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 241
DB 244 TAGACAGTGTGAAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 303
QY 242 TGCAGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 301
DB 304 TGCAGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 363
QY 302 ACGGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 348
DB 364 TAGTCCCGTTGCTTACTGGGCGCAAGGAGTCTGTGTCACCGCTCTCT 410

RESULT 2
US-08-452-164A-56
; Sequence 56, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
; US-08-452-164A-56

Query Match 73.3%; Score 257.4; DB 2; Length 413;
Best Local Similarity 83.9%; Pred. No. 3.7e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGCTGGTGGAGTCTGGGGAGGCGTTGTGACAGCTGGAAGGTCCTGAGACTCT 61
DB 64 AAGTGAAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGAGCTGGAGGTCCTGAAACTCT 123
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGCTC 121
DB 124 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGCTC 183
QY 122 CGGCAAGGCTGGAGTCTGGGAGGCGTTGTGAGTAGTGTGTTAGTACCTACTATT 181
DB 184 CGGAGAGGCTGGAGTCTGGGAGGCGTTGTGAGTAGTGTGTTAGTACCTACTATT 243
QY 182 TAGACACTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 241
DB 244 TAGACAGTGTGAAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 303
QY 242 TGCAGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 301
DB 304 TGCAGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 363
QY 302 ACGGAGTGTGAGGCGGATTCACCTTCAGAGACAATAGTAGAAGACACCTATACC 348
DB 364 TAGTCCCGTTGCTTACTGGGCGCAAGGAGTCTGTGTCACCGCTCTCT 410

RESULT 3
US-08-591-51
; Sequence 15, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
```


Db 119 CCGTGCAGCCTCTCGATTCGCTTTTCAGTAGCTATGCCATGCTCTGGGTGCGCCAGCTCT 178
QY 122 CGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
Db 179 CAGAGAAGGCTGAGTGGGTGCGAGAAATTAGTAGTGGTAAATTACGCCCTACTATC 238
QY 182 TAGACACTGTGCAGGCGCGATTCACCTCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 239 AAGACACTGTGACGGCGGATTCACCTCTCCAGAGACAATGCCAAGAACCCCTGTACC 298
QY 242 TGCRAATGAACCTCTTGAGAGCGGAGGACAGACCGGTGTATTACTGTGCAAGACATAACT 301
Db 299 TGGAAATGAGCAGCTGAGTGGGTCTGAGGACAGCGCCATGTATTACTGTGCAAGGAGGACT 358
QY 302 ACGG-----CAGTTTCTCTACTGGGCCAAGGACACTACACTGCTTCT 348
Db 359 ACGGTATCCCGGCTGGTTTCTTACTGGGGCCAAAGGACTCTGTGCTCTCT 414

RESULT 11

US-08-672-176A-3
; Sequence 3, Application US/08672176A
; Patent No. 5908925
; GENERAL INFORMATION:
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
; TITLE OF INVENTION: Specificity for Glycated Albumin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Exocell, Inc.
; STREET: 3508 Market Street, suite 420
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS 4.0 or better
; SOFTWARE: Wordperfect, Version 5.2
; CURRENT APPLICATION DATA: US/08/672.176A
; APPLICATION NUMBER: unknown
; FILING DATE: unknown
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Robert S.
; REGISTRATION NUMBER: unknown
; REFERENCE/DOCKET NUMBER: E1043/20002
; TELEPHONE: 215-567-2010
; TELEFAX: 215-751-1142
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs/120 amino acid residues
; TYPE: nucleic acid/amino acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: humanized A717 heavy chain variable region
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: synthetic
; ORGANISM: N/A
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A

; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: plasmid
; LIBRARY: N/A
; CLONE: PHUA717VH-1
; POSITION IN GENOME: N/A
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS: human framework regions; murine CDRs
; NAME/KEY: FR-1; CDR-1; FR-2; CDR-2; FR-3; CDR-3; FR-4
; LOCATION: aa#1-30; aa#31-35; aa#36-49; aa#50-66;
; LOCATION: aa#67-98; aa#99-109; aa#110-120
; IDENTIFICATION METHOD: similarity to known sequences
; OTHER INFORMATION: antigen is human glycated albumin
; PUBLICATION INFORMATION: N/A
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 3:
US-08-672-176A-3

Query Match 68.5%; Score 240.6; DB 2: Length 360;
Best Local Similarity 82.3%; Pred No. 1.5e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGCAGCTGTGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGCCCTTGAGACTCT 61
Db 2 AGGTGCAGCTGTGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGCCCTTGAGACTCT 61
QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTTCGCCAGGCTC 121
Db 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTTCGCCAGGCTC 121
QY 122 CGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
Db 122 CTGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
QY 182 TAGACACTGTGCAGGCGCGATTCACCTCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 182 CAGACAGTGTGAAGGCGGATTCACCTCTCCAGAGACAATTCGAAGAACAACGTTGTACC 241
QY 242 TGCRAATGAACCTCTTGAGAGCGGAGGACAGACCGGTGTATTACTGTGCAAGA----- 294
Db 242 TGCRAATGAACCTCTTGAGAGCGGAGGACAGACCGGTGTATTACTGTGCAAGAAGTGT 301
QY 295 --CATAACTACGCGAGTCTTCTTACTGGGGCCAAAGGACTACAGTACTGTTTC 347
Db 302 ATCTTTATTACTATCTGCTATGACTACTGGGTCAAGGAACACACACTCACCCTC 356

RESULT 12
US-08-672-176A-5
; Sequence 5, Application US/08672176A
; Patent No. 5908925
; GENERAL INFORMATION:
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
; TITLE OF INVENTION: Specificity for Glycated Albumin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Exocell, Inc.
; STREET: 3508 Market Street, suite 420
; CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM: diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: PC
OPERATING SYSTEM: DOS 4.0 or better
SOFTWARE: Wordperfect, Version 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,176A
FILING DATE: unknown
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Silver, Robert S.
REGISTRATION NUMBER: unknown
REFERENCE/DOCKET NUMBER: E1042/20002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2010
TELEFAX: 215-751-1142
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs/240 amino acid residues
TYPE: nucleic acid/amino acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: humanized A717 immunoglobulin single-chain Fv
HYPOTHETICAL: yes
ANTI-SENSE: no
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE: synthetic
ORGANISM: N/A
STRAIN: N/A
INDIVIDUAL ISOLATE: N/A
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: plasmid
LIBRARY: N/A
CLONE: pHuA717ScFv-1
POSITION IN GENOME: N/A
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE: HuA717VH-1 linked to HuA717VL
NAME/KEY: HuA717VH; linker: HuA717VL
LOCATION: aa# 1-120; aa# 121-133; aa# 134-240
IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycosylated albumin
PUBLICATION INFORMATION: N/A
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5:
US-08-672-176A-5

Query Match 68.5%; Score 240.6; DB 2; Length 720;
Best Local Similarity 82.3%; Pred. No. 2.1e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTTGAAGGTCCTCGAGACTCT 61
|||||
Db 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTTGAAGGTCCTCGAGACTCT 61
|||||
QY 62 CTTGTGCAGCCCTCTGGATTACCTTCAGTAGCTATGACATGTCCTGGTTGCGCAGGCTC 121
|||||
Db 62 CTTGTGCAGCCCTCTGGATTACCTTCAGTAGCTATGACATGTCCTGGTTGCGCAGGCTC 121
|||||
QY 122 CGGGCAAGGCTGTGGAGTGTGGCGCAAGTGTAGTAGTGTGGTGTGCTAGCCTACTATT 181
|||||
Db 122 CTTGGCAAGGCTGTGGAGTGTGGCGCAAGTGTAGTAGTGTGGTGTGCTAGCCTACTATT 181
|||||
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAAATAGTAAGACACCTTATAC 241
|||||
Db 182 CAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAAATAGTAAGACACCTTATAC 241
|||||
QY 242 TGAATGAATGAACTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGA- 294
|||||
Db 242 TGAATGAATGAACTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGAATGGTT 301
|||||
QY 295 --CATAACTACGCGAGTTTGTCTTACTGGGCGCAAGGACTACAGTGACTGTTC 347
|||||
Db 302 ATCTTTATTACTATGCTATGGACTACTGGGCTCAGGAACACAGTACCGTCTC 356
|||||
RESULT 13
US-08-475-000-15
; Sequence 15, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 635-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
; US-08-475-000-15

Query Match 68.3%; Score 239.8; DB 1; Length 357;
Best Local Similarity 82.2%; Pred. No. 2.8e-71;
Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

Qy	2	AGGTGCAGCTGGTGGAGCTCTGGGGGAGGCGCTGTGTGCAGCGCTGGAAGGTCCTCTGAGACTCT	61
Db	2	AGGTGAAGGTTGTGGAGCTCTGGGGGAGTCTTACTGAGGCGCTGGAGGTCCTCTGAAACTCT	61
Qy	62	CCTGTGCAGCCCTCTGGATTACACTTCAGTAGCTATGACATGCTCTGGTTCGCCAGGCTC	121
Db	62	CCTGTGCAGCCTCTGGATTCACTTTTCAGTAGTATACCATGCTCTGGTTCGCCAGACTC	121
Qy	122	CGGCAAGGCTCTGGAGTGGGTCGCAAAAGCTTAGTAGTGGTGGTGTAGCACTACTATT	181
Db	122	CGGAAAGCGCTGGAGTGGGTGCAACCAATAGTAGTGGTGGTGTAACTACTATC	181
Qy	182	TAGACACTGTGCAGGGCGGATTCAACATCTCCAGAGACAATAGTAGAACAACCCCTATACC	241
Db	182	CAGACAGTGTGAAGGTCGATTCACGTCTCCAGAGACAATGCCATGACGCCCTGTACC	241
Qy	242	TGCAAAATGAACCTCTGTAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGACA	296
Db	242	TGCAAAATGACAGCTCTGAGTCTGAGGACACGSCCTGTATTACTGTGCAAGATACGGGG	301
Qy	297	-TAACTAGCCGAGTTTTCCTTACTGGGGCAAGGGACTACAGTGACTGTTTCT	348
Db	302	CTGGTGACGCTCTGTTTGTCTTACTGGGGCAAGGGACTCTGGTCACAGTTTCT	354

Search completed: October 11, 2001, 15:14:12
Job time: 4999 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2001, 11:57:35 ; Search time 31.63 Seconds
(without alignments)
281.771 Million cell updates/sec

Title: US-08-791-391A-2
Perfect score: 616
Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNYGSFAYWGQGTIVTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	507	82.3	119	2 S31108	Ig heavy chain - h
2	503	81.7	119	2 C36005	Ig heavy chain v r
3	503	81.7	119	2 S31107	Ig heavy chain - h
4	503	81.7	121	2 S19666	Ig heavy chain - h
5	503	81.7	127	2 S38489	Ig heavy chain - h
6	503	81.7	140	2 S31588	Ig heavy chain v r
7	502	81.5	140	2 S31586	Ig heavy chain v r
8	501	81.3	134	2 S31679	Ig heavy chain v r
9	500.5	81.2	122	2 E36005	Ig heavy chain v r
10	499	81.0	132	2 S31603	Ig heavy chain v r
11	498.5	80.9	122	2 S31117	Ig heavy chain - h
12	498.5	80.9	128	2 S48797	Ig heavy chain v r
13	498	80.8	121	2 G36005	Ig heavy chain v r
14	494	80.2	119	2 D36005	Ig heavy chain v r
15	494	80.2	119	2 F36005	Ig heavy chain v r
16	494	80.2	123	2 S31114	Ig heavy chain - h
17	494	80.2	138	2 S31666	Ig heavy chain v r
18	493.5	80.1	120	2 S48798	Ig heavy chain v r
19	492.5	80.0	114	2 S46392	Ig heavy chain v r
20	492	79.9	117	2 S78486	Ig heavy chain v r
21	492	79.9	160	2 S05271	Ig heavy chain pre
22	491.5	79.8	114	2 S46390	Ig heavy chain v r
23	490	79.5	121	2 I55673	Ig heavy chain - h
24	488.5	79.3	137	2 S31701	Ig heavy chain v r
25	487	79.1	134	2 S31699	Ig heavy chain v r
26	485.5	78.8	118	2 S31116	Ig heavy chain - h
27	485.5	78.8	140	2 S70442	Ig heavy chain pre
28	485	78.7	133	2 A49028	Ig heavy chain v r
29	485	78.7	143	2 S23624	Ig heavy chain v r

ALIGNMENTS

RESULT 1
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31108
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62956
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 507; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 2e-39;
Matches 98; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWVRQAPGKGLVWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLVWVSAITSGGSTYY 60
Qy 61 LDTVGQRTISRDNSKNTLYIQMNSLRADFTAVYCA--RHNYGSFAYWGQGTIVTVSS 117
:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADFTAVYCAKDRRLTGTFYWGQGTIVTVSS 119

RESULT 2
C36005
Ig heavy chain v region (30p1) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schröder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571
A:Accession: C36005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

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Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.5e-39;
Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARH-NYGS-FAYWGQTTVTSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKADAGWGFYDWGQGLTVTVSS 119

RESULT 3
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62955
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.5e-39;
Matches 98; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARHNYGS--FAYWGQTTVTSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKDPGASYYFYDWGQGLTVTVSS 119

RESULT 4
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MA>
A:Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 4.6e-39;
Matches 98; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60

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Db 1 QVQLVQSGGGVVPQGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVSDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARHNY---GSFAYWGQTTVTYS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKTYSGSGWGFYDWGQGLTVTVS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 S 117
Db 121 S 121

RESULT 5
S38489
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z23028; NID:g414025; PIDN:CAA80563.1; PID:g414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 127;
Best Local Similarity 77.2%; Pred. No. 4.8e-39;
Matches 98; Conservative 6; Mismatches 11; Indels 12; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGGGVVPQGRSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARH-----NYGSFAYWG 108
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKEGPPASDYDSSGYYSFDFWG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 QGTTVT 115
Db 121 QGTLTV 127

RESULT 6
S31588
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CU>
A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 140;
Best Local Similarity 80.2%; Pred. No. 5.4e-39;
Matches 97; Conservative 11; Mismatches 9; Indels 4; Gaps 2;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:00 ; Search time 17.83 Seconds
(without alignments)
224.784 Million cell updates/sec

Title: US-08-791-391A-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNGSFAYWGQGTITVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	481.5	78.2	122	1 HV3G_HUMAN	P01768 homo sapien
2	456	74.0	121	1 HV3J_HUMAN	P01771 homo sapien
3	453	73.5	119	1 HV3I_HUMAN	P01770 homo sapien
4	451.5	73.3	136	1 HV16_MOUSE	P01783 mus musculus
5	449.5	73.0	126	1 HV3K_HUMAN	P01772 homo sapien
6	446	72.4	117	1 HV3C_HUMAN	P01764 homo sapien
7	442.5	71.8	114	1 HV3B_HUMAN	P01763 homo sapien
8	441.5	71.7	116	1 HV3T_HUMAN	P01781 homo sapien
9	441.5	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
10	428	69.5	117	1 HV55_MOUSE	P18526 mus musculus
11	424	68.8	115	1 HV3F_HUMAN	P01767 homo sapien
12	423	68.7	119	1 HV3L_HUMAN	P01773 homo sapien
13	418.5	67.9	116	1 HV05_CARAU	P19181 carassius a
14	418	67.9	117	1 HV54_MOUSE	P18525 mus musculus
15	415.5	67.5	119	1 HV37_MOUSE	P01807 mus musculus
16	415.5	67.5	119	1 HV40_MOUSE	P01810 mus musculus
17	415	67.4	115	1 HV3D_HUMAN	P01765 homo sapien
18	415	67.4	120	1 HV3E_HUMAN	P01766 homo sapien
19	410.5	66.6	119	1 HV3M_HUMAN	P01774 homo sapien
20	408.5	66.3	119	1 HV3N_HUMAN	P01775 homo sapien
21	407.5	66.2	120	1 HV3U_HUMAN	P01782 homo sapien
22	407.5	66.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	406	65.9	117	1 HV02_CANFA	P01785 canis fami
24	405.5	65.8	114	1 HV01_CANFA	P01784 canis fami
25	404	65.6	115	1 HV32_MOUSE	P01801 mus musculus
26	403.5	65.5	119	1 HV38_MOUSE	P01808 mus musculus
27	402.5	65.3	122	1 HV20_MOUSE	P01789 mus musculus
28	402	65.3	113	1 HV30_MOUSE	P01799 mus musculus
29	400	64.9	142	1 HV01_RAT	P01805 rattus norv
30	399	64.8	118	1 HV39_MOUSE	P01809 mus musculus
31	397	64.4	113	1 HV27_MOUSE	P01796 mus musculus
32	395.5	64.4	97	1 HV56_MOUSE	P18527 mus musculus
33	395.5	64.2	111	1 HV35_MOUSE	P01804 mus musculus

ALIGNMENTS

RESULT 1

```

HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

```

Query Match 78.2%; Score 481.5; DB 1; Length 122;
Best Local Similarity 74.6%; Pred. No. 9.9e-42;
Matches 91; Conservative 12; Mismatches 14; Indels 5; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKGLEWYAKVSSGGSTYY 60

Db 1 QVELVESGGGVVQPGKSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWYAVTSYGBBKYY 60

Qy 61 LDTVOGRFTISRDNKNLYLQMNLSRAEDTAVYYCARH-----NYGSFAYWGQGTITV 115

Db 61 ABSVKGRTISRDNKSKLYLQMNLSRAEDTAVYYCARDPLRYGFRFYWGQGTITV 120

Qy 116 SS 117

Db 121 SS 122

RESULT 2

HV3J_HUMAN

ID HV3J_HUMAN STANDARD; PRT; 121 AA.

AC P01771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V-III REGION HIL.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 cryoimmunoglobulin IgG H1L";
 RL Biochemistry 18:553-560(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR; A02054; GIHUHL.
 DR HSSP; P01772; 2IG2.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT DISULFID 22 96
 FT NON_TER 119 119
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 74.0%; Score 456; DB 1; Length 121;
 Best Local Similarity 73.6%; Pred. No. 3.6e-39;
 Matches 89; Conservative 9; Mismatches 19; Indels 4; Gaps 1;
 QY 1 QVQLVSGGVPQGRSLRSCAASGFTSSYDMVSRQAPGKGLWVAKVSSGGSTYY 60
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 1 QVQLVAGGVPQGRSLRSCAASGFTSSYDMVSRQAPGKGLWVAVTWNGSRITY 60
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 LDTVQGRFTISRDNKNTLYLNMSLRADTAVYYCARH----NYGSFAYWGQGTVTVS 116
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 61 GDSVKGRTISRDNKNTLYLNMSLRADTAVYYCARPDILTAFSDYWGQGLVTVS 120
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 117 S 117
 DB 121 S 121

RESULT 3
 HV31_HUMAN STANDARD; PRT; 119 AA.
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION NIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=7070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR; A02053; GIHUNI.

DR HSSP; P01772; 2IG2.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT DISULFID 22 96
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6E5E165B CRC64;

Query Match 73.5%; Score 453; DB 1; Length 119;
 Best Local Similarity 75.6%; Pred. No. 7e-39;
 Matches 90; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVSGGVPQGRSLRSCAASGFTSSYDMVSRQAPGKGLWVAKVSSGGSTYY 60
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 1 QVQLVSGGVPQGRSLRSCAASGFTSSYDMVSRQAPGKGLWVAVMSYBGBKKHY 60
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 LDTVQGRFTISRDNKNTLYLNMSLRADTAVYYCARHNYGS--FAYWGQGTVTVS 117
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 61 ADSVNGRTISRDNKNTLYLNMSLRADTAVYYCARIRDTAMFFAHWGQGLVTVSS 119

RESULT 4
 HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adetugbo K., Milstein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants."
 RL Nature 265:299-304(1977).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00522; AAD15290.1; -.
 DR PIR; A02066; GMS21.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 16
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
 FT DOMAIN 115 119 D SEGMENT.
 FT DOMAIN 120 136 JH4 SEGMENT.
 FT DISULFID 38 112
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).
 FT CONFLICT 115 115 W -> H (IN REF. 2).
 FT CONFLICT 120 120 Y -> W (IN REF. 2).

FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 73.3%; Score 451.5; DB 1; Length 136;
Best Local Similarity 74.8%; Pred. No. 1.1e-38;
Matches 89; Conservative 12; Mismatches 15; Indels 3; Gaps 2;
QY 2 VOLVESGGVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTYYL 61
DB 18 VOLVESGGGLVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTLHYA 77
QY 62 DTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGTITVTVSS 117
DB 78 DTVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGTITVTVSS 136

RESULT 5
HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[2]

X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Delsenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
and 1.0-A resolution.";
RN J. Mol. Biol. 141:369-391(1980).
DR PIR; A02055; GIHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; 3D-structure.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT TURN 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113

FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 73.0%; Score 449.5; DB 1; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.7e-38;
Matches 90; Conservative 10; Mismatches 17; Indels 9; Gaps 2;
QY 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTYY 60
DB 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGT 111
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQGT 120

QY 112 TVTVSS 117
DB 121 PVTVSS 126

RESULT 6

HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RN Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
[2]

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CC -----

DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 72.4%; Score 446; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.5e-38;
Matches 84; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTYY 60
DB 20 EVQLLESGLLVQPGSRSLRLSCAASGFTFSYDMVWVRQAPGKLEWVAKVSSGGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
DB 80 GDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAR 117

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CC      MACROGLOBULIN.
DR      PIR; A02064; M3HUGL.
DR      HSSP; P01772; 2IG2.
DR      InterPro; IPR003006; -.
DR      Pfam; PF00047; Ig_1.
KW      Immunoglobulin V region.
FT      NON_TER 116 116
SQ      SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match          71.7%; Score 441.5; DB 1; Length 116;
Best Local Similarity 71.8%; Pred.No. 9.7e-38;
Matches 84; Conservative 12; Mismatches 20; Indels 1; Gaps

QY      1 QVQLVESGGGVQPGRSRLRSCAASGETFSYSDMSWRQAPGKLEWVAKVSGGGSTYY 60
       :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1 EVQLVESGGDLVPGRSLRSCAASGFPEBBLGTWTWRQAPGKLEWVANIKZBSZZBY 60

QY      61 LDTVGRRFTISRDNKNLTLYLQMNSLRADTAVYICCARHNYSGFAYWGOGTTVTVSS 117
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       61 VDSVKRGFTISRDNAKNLSLYLQMNSLRVEDTALYICAR-GWGGGDYWGOGTLTVTVTST 116

RESULT      9
HV3H_HUMAN  STANDARD;      PRT;      122 AA.
AC          HV3H_HUMAN
ID          AC P01769;
DT          DT 21-JUL-1986 (Rel. 01, Created)
DD          DD 21-JUL-1986 (Rel. 01, Last sequence update)
OT          OT 15-JUL-1999 (Rel. 38, Last annotation update)
DE          DE IG HEAVY CHAIN V-III REGION GA.
OS          OS Homo sapiens (Human).
OC          OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
QC          QC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```

CA		NCBI_1axid=9606,
RN	[1]	
RP	SEQUENCE.	
RX	MEDLINE=741175307; PubMed=4208843;	
RT	Florent G., Lehman D., Putnam F.W.;	
RR	"The switch point in mu heavy chains of human IgM immunoglobulins.";	
RL	Biochemistry 13:2482-2498(1974).	
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.	
DR	PIR: A02052; M3HUGA.	
DR	HSP; P01772; 2IG2.	
DR	InterPro: IPR003006; -.	
DR	Pfam: PF00047; Ig; 1.	
KW	Immunoglobulin V region.	
FT	MOD_RES 1 1	
FE	NON_TER 122 122	PYROLIDONE CARBOXYLIC ACID.
SQ	SEQUENCE 122 AA; 13166 MW; 74ESB6959884100A CRC64;	

[illegible]

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AC #18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J03052; HVMS34.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 69.5%; Score 428; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 2.2e-36;
Matches 80; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 79
Qy 61 LDTVGQRTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
Db 80 PDTVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAR 117

RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPIC, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR: A02050; A2HUBU.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
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SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 68.8%; Score 424; DB 1; Length 115;
Best Local Similarity 69.2%; Pred. No. 5.5e-36;
Matches 81; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 1 EVQLVETGGGLVPGGSLRLSCAASGFTVBSHNSWVRQAPGKALZWSAIVR-GGTYIY 59
Qy 61 LDTVGQRTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYGSFAYWGQGTITVSS 117
Db 60 ADSVKGRTISRDRSRVTYQLQMSLRAEDTAVYYCAR-DLAAARLFKGKTTVTSS 115

RESULT 12
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR: A02056; ALHUBR.
DR HSSP: P01772; 2IG2.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 68.7%; Score 423; DB 1; Length 119;
Best Local Similarity 69.5%; Pred. No. 7.2e-36;
Matches 82; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 1 QVQLVESGGGVQAGTSLRLSCTSAFNLSDYAMHWVRQAPGKGLZVVALISYGGSBTY 60
Qy 61 LDTVGQRTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--HNYGSFAYWGQGTITVSS 116
Db 61 ADSVKGRTISRDRSRVTYQLQMSLRAEDTAVYYCAKLIAVAGTRBFWGQGTITVSS 118

RESULT 13
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinidae; Carassius.
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Job time: 403 sec

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Db 61 DSVKGRFTISRDNSKNTLYQMNSLRADETAMYYCAGGGGGLGLGWGGTTLTVSS 116
RESULT 2
Q9UL90 ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035024; AAD56260.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 77.1%; Score 475; DB 4; Length 113;
Best Local Similarity 79.5%; Pred. No. 1.4e-42;
Matches 93; Conservative 6; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMSVWRQAPGKLEWVAVIRYDGSNKYY 60
Db 1 EVQLVESGGGVQPGKSLRSCAASGFTSSYGMHWVRQAPGKLEWVAVIRYDGSNKYY 60

QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRADETAVYYCAHNYGSFYWGQGTTLTVSS 117
Db 1 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYYCAK----DLNFWGGTTLTVSS 113

RESULT 3
Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; -.

Query Match 77.1%; Score 475; DB 4; Length 113;
Best Local Similarity 79.5%; Pred. No. 1.4e-42;
Matches 93; Conservative 6; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMSVWRQAPGKLEWVAVIRYDGSNKYY 60
Db 1 EVQLVESGGGVQPGKSLRSCAASGFTSSYGMHWVRQAPGKLEWVAVIRYDGSNKYY 60

QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRADETAVYYCAHNYGSFYWGQGTTLTVSS 117
Db 1 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYYCAK----DLNFWGGTTLTVSS 113
```

```
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 76.9%; Score 474; DB 4; Length 121;
Best Local Similarity 76.0%; Pred. No. 1.9e-42;
Matches 92; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMSVWRQAPGKLEWVAVIRYDGSNKYY 60
Db 1 EVQLVESGGGVQPGKSLRSCAASGFTSSYGMHWVRQAPGKLEWVAVIRYDGSNKYY 60

QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRADETAVYYCAHNYGSFYWGQGTTLTVSS 116
Db 61 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYYCAKGVTTIYDRFDIWGGTMTVTS 120

QY 117 S 117
Db 121 S 121

RESULT 4
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 75.4%; Score 464.5; DB 4; Length 147;
Best Local Similarity 71.4%; Pred. No. 2.4e-41;
Matches 90; Conservative 9; Mismatches 18; Indels 9; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMSVWRQAPGKLEWVAVIRYDGSNKYY 60
Db 1 QVHLVESGGGVQPGKSLRSCAASGFTSSYGMHWVRQAPGKLDWVALISYDGSQYY 60

QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRADETAVYYCAHNYGSFYWGQGT 111
Db 61 AGSVKGRFTISRDNSKNTLYQMNSLRADETAVYYCAKDGNYFSDYGVYAGIDYWGQGT 120

QY 112 TVTVSS 117
Db 121 LVTVSS 126
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RESULT 5
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
  DOMAIN.
CC EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 118;
Best Local Similarity 78.2%; Pred. No. 4.8e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps 2;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGLVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 59
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNTGSFA--YWGQGTITVSS 117
Db 60 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARDRGCEFLFDYWGQGTITVSS 118

RESULT 6
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
  DOMAIN.
CC EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.

Query Match 74.6%; Score 459.5; DB 4; Length 112;
Best Local Similarity 77.0%; Pred. No. 5.7e-41;
Matches 87; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFDDYGMWVRQAPGKLEWVSNWNGSGTGY 60
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNTGSFA--YWGQGTITV 113
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARRRY-ALDYWGQGTITV 112

RESULT 8
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNTGSFA--YWGQGTITV 115
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICAKDRGLVGYFDYWGQGTITV 120

Qy 116 SS 117
Db 121 SS 122
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DR InterPro; IPR003596; -.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D411366545B8 CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNTGSFA--YWGQGTITV 115
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICAKDRGLVGYFDYWGQGTITV 120

Qy 116 SS 117
Db 121 SS 122

RESULT 7
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : isolation from a
  human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 74.6%; Score 459.5; DB 4; Length 112;
Best Local Similarity 77.0%; Pred. No. 5.7e-41;
Matches 87; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFDDYGMWVRQAPGKLEWVSNWNGSGTGY 60
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNTGSFA--YWGQGTITV 113
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARRRY-ALDYWGQGTITV 112

RESULT 8
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035023; AAD56259.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 74.4%; Score 458.5; DB 4; Length 118;
Best Local Similarity 76.9%; Pred. No. 7.7e-41;
Matches 90; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYQMNSLRADTAVYYC-----ARHNYGSFAY 106
Db 61 DYAAPVKGRLTISRDSSKNTLYLRMSLKTADTAVYYCTGTTMIIVITSSKRTSFY 120
QY 107 WGQGTIVTVSS 117
Db 121 WGQGTIVTVSS 131

RESULT 9
QYUL88 ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 67.2%; Score 414; DB 4; Length 95;
Best Local Similarity 82.1%; Pred. No. 2.8e-36;
Matches 78; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 VOLVESGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYYL 61
Db 1 VQLESGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
QY 62 DTVQGRFTISRDNKNTLYQMNSLRADTAVYYC 96
Db 61 DSVKGRFTISRDNKNTLYQMNSLRADTAVYYC 95

RESULT 11
QYQYFO ID Q9QYFO PRELIMINARY; PRT; 298 AA.
AC Q9QYFO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035023; AAD56259.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 74.4%; Score 458.5; DB 4; Length 118;
Best Local Similarity 76.9%; Pred. No. 7.7e-41;
Matches 90; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYQMNSLRADTAVYYC-----ARHNYG-SFAYWGQGTIVTVSS 116
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAVYYCARGDSEAFDVGQGTIVTVSS 117

RESULT 9
QYUL88 ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035026; AAD56262.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 68.0%; Score 419; DB 4; Length 131;
Best Local Similarity 65.6%; Pred. No. 1.2e-36;
Matches 86; Conservative 10; Mismatches 21; Indels 14; Gaps 2;

QY 1 QVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSS--GGGST 58
Db 1 EVLTSGGGVQPGRLSLRSLSCAASGFTFSSYDMSWVRQAPGKLEWVAKVSSGGGST 60
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RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a plaque display subtraction
RL method.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR NCBI_TaxID=9606;
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 65.5%; Score 403.5; DB 11; Length 298;
Best Local Similarity 64.4%; Pred. No. 1.4e-34;
Matches 76; Conservative 20; Mismatches 21; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWVRQAPGKGLVWAKVSSGGSTYY 60
Db 40 QVQLQSGGLVPGGSLKSLCAASGDFSRKWMVWVRQAPGKGLVWAKVSSGGSTYY 99
Qy 61 LDTVQGRFTISRDNSKNTLYLQMNSLRADTAIVYCARHN-YGSPAYWGQGTIVTVSS 117
Db 100 TPSLKDKEFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYGHAYWGQGTIVTVSS 157

RESULT 12
Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; -.
DR InterPro; IPR003600; -.
DR Pfam; PF00047; Ig; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SMART; SM00410; IG_like; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 65.5%; Score 403.5; DB 11; Length 437;
Best Local Similarity 69.8%; Pred. No. 2.3e-34;
Matches 81; Conservative 12; Mismatches 20; Indels 3; Gaps 2;

Qy 2 VOLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWVRQAPGKGLVWAKVSSGGSTYYL 61
Db 1 VOLQESGGLVPGGSLKSLCAASGFTSSYAMSVWRQTPKRLVWASFS-SGGIYYT 59
Qy 62 DTVQGRFTISRDNSKNTLYLQMNSLRADTAIVYCARHNYGSPAYWGQGTIVTVSS 117
Db 60 DSVKGRFTIYKDRNILLSQMSLSRSEDTAMYYCARDGYS--AYWGPTLTVTSA 113
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RESULT 13
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035022; AAD56258.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 62.1%; Score 382.5; DB 4; Length 124;
Best Local Similarity 58.9%; Pred. No. 7.9e-33;
Matches 73; Conservative 19; Mismatches 25; Indels 7; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTSSYDMSVWVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQLVESGAEVKPGASVKVSKASSYTFSSYHMHVWRQAPGQGLEWMGIINPSGGSTSY 60
Qy 61 LDTVQGRFTISRDNSKNTLYLQMNSLRADTAIVYCARHNY-----GSFAYWGQGTIV 113
Db 61 AOKFGQGRVTMTDSTSTVYMELSLSRSDTAIVYCARGLYVVPAAFRFDYWGQGTIV 120
Qy 114 TVSS 117
Db 121 TVSS 124

RESULT 14
Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035027; AAD56263.1; -.
DR InterPro; IPR003006; -.

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DR InterPro: IPR003600; -.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00410; IG_like; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 60.4%; Score 372; DB 4; Length 104;
Best Local Similarity 70.2%; Pred. No. 8.1e-32;
Matches 73; Conservative 9; Mismatches 14; Indels 8; Gaps 2;

QY 22 CAASGTFSSYDMVSRQAPGKGLWAKVSGGGSTYYLDTVQGRFTISRDNKNTLYL 81
   |||||  |  |||||  |||||  :  ||  |  :  |||||  |||||  :  |||
Db 1 CAASGTFDDYAMHWVSRQAPGKGLWVSGISWNSGSGIGYADSVKGRFTISRDNKNSLYL 60
QY 82 QMNSLRAEDTAVTYCARHNY---GS-----FAYWGQGTVTYVSS 117
   |||||  |||||  |||||  ||  ||  |  :  ||||  |||||
Db 61 QMNSLRAEDTALYCAKANYGSGSYTYEYFQHWGQGTLYTVSS 104

RESULT 15
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOBULBULIN HEAVY CHAIN (FRAGMENT).
GN IGH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Zafiroopoulos A., Kandilgiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RT "Induction of somatic mutations in human B cells by in vitro
RT immunization.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ132560; CAB65078.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;

Query Match 59.4%; Score 366; DB 4; Length 112;
Best Local Similarity 67.6%; Pred. No. 3.8e-31;
Matches 71; Conservative 10; Mismatches 12; Indels 12; Gaps 1;

QY 18 LRLSCAAGTFSSYDMVSRQAPGKGLWAKVSGGGSTYYLDTVQGRFTISRDNKSN 77
   |||||  |||||  |||||  |||||  :  ||  |  :  |||||  |||||  :  |||
Db 1 LRLSCAAGTFSSYAITVSRQAPGKGLWVSSINATSGTTDYADSVKGRFTISRDNKSN 60
QY 78 TLYLQMSLRAEDTAVTYCARHNYGSFA-----YWGQG 110
   |||||  |||||  |||||  ||  ||  |  :  ||||  |||||
Db 61 TLYLQMSLRAEDTAVTYCARDGGHIVAVPTAVLLIFTGDYWGQG 105

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2001, 11:45:50 ; Search time 44.8 Seconds

(without alignments)
158.326 Million cell updates/sec

Title: US-08-791-391a-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVVQPGRLRL.....RHNGSFAYWGQQTIVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
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- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	117	19 AAW76001	Vitaxin antibody h
2	616	100.0	117	22 AAB61359	Vitaxin heavy chain
3	552	89.6	117	19 AAW76003	LM609 antibody hea
4	552	89.6	117	22 AAB61361	Antibody LM609 hea
5	539	87.5	117	18 AAW27526	Heavy chain variab
6	539	87.5	239	20 AAW73874	Human antiFc epsil
7	539	87.5	242	20 AAW73876	Human antiFc epsil
8	536	87.0	117	20 AAY06381	Murine monoclonal
9	525	85.2	130	20 AAY06379	Murine monoclonal
10	523.5	85.0	118	19 AAW57591	Chimeric antibody
11	523.5	85.0	118	20 AAW89636	Human antibody hea

12	523.5	85.0	118	21 AAY77512	Peptide seq ID No:
13	523.5	85.0	118	22 AAB76890	Human antibody H c
14	523.5	85.0	118	22 AAB76909	Human antibody H c
15	523.5	85.0	118	22 AAB76928	Human antibody H c
16	523.5	85.0	137	19 AAW57603	Chimeric antibody
17	523.5	85.0	137	20 AAW89635	Human antibody hea
18	523.5	85.0	137	21 AAY77514	Peptide encoded by
19	517.5	84.0	139	15 AAR52823	Humanised murine K
20	517.5	84.0	139	16 AAR70471	Humanised anti-KC-
21	517.5	84.0	240	20 AAY02472	A single chain ant
22	517	83.9	121	20 AAW86122	Protein sequence o
23	514	83.4	245	22 AAB67620	Human leukocyte an
24	509.5	82.7	139	18 AAW21652	Humanised reshaped
25	509	82.6	119	22 AAB62088	Human Vh consensus
26	509	82.6	119	22 AAB60401	Consensus human he
27	509	82.6	119	22 AAB61586	Human variable hea
28	509	82.6	240	21 AAY15124	Anti-human CTLA-4
29	509	82.6	240	21 AAY15125	Anti-murine CTLA-4
30	508	82.5	121	20 AAW86120	Protein sequence o
31	508	82.5	138	21 AAY32406	Mouse anti-verotox
32	505	82.0	113	19 AAW70621	Human consensus se
33	505	82.0	113	21 AAY82347	Human consensus fr
34	503.5	81.7	443	18 AAW13564	Humanised anti-L-S
35	503	81.7	117	20 AAW86137	Protein sequence o
36	502	81.5	119	14 AAR32240	Humanised MAB hea
37	501.5	81.4	120	18 AAW27553	Human Ab heavy cha
38	501.5	81.4	281	18 AAW27560	Consensus single c
39	500.5	81.2	118	22 AAB67508	Light chain variab
40	500.5	81.2	118	22 AAB67513	Heavy chain variab
41	500.5	81.2	131	18 AAW13520	Anti-melanoma anti
42	500.5	81.2	143	21 AAY82629	Human PTHrP monocl
43	500	81.2	117	19 AAW48866	Chimeric humanized
44	500	81.2	117	20 AAW86135	Protein sequence o
45	500	81.2	264	19 AAW73049	Humanised A33 SCAB

ALIGNMENTS

RESULT 1
AAW76001
ID AAW76001 standard; Protein; 117 AA.
XX
AC AAW76001;
XX
XX
DT 02-NOV-1998 (first entry)
XX
DE Vitaxin antibody heavy chain variable region protein fragment.

XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis.
XX
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
XX
DR N-PSDB; AAW49820.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 1; Fig 1a; 129pp; English.
 XX This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 616; DB 19; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.5e-49;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWVAKVSSGGSTYY 60
 |||||
 Db 1 qvqlvesgggvqpgrslrlscaasgftfssydmwvrrqapkgkglewvkvssggstyy 60
 |||||
 QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTVVYCARHNYGSFAYWGOGTTVTSS 117
 |||||
 Db 61 ldtvqgrftisrdnsnkntlylqmslraedtavvycarhnygsfaywgogttvtvss 117
 |||||

RESULT 2

AAB61359
 ID AAB61359 standard; protein; 117 AA.

XX
 AC AAB61359;

XX 03-APR-2001 (first entry)

XX Vitaxin heavy chain variable region protein.

XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 616; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.5e-49;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWVAKVSSGGSTYY 60
 |||||
 Db 1 qvqlvesgggvqpgrslrlscaasgftfssydmwvrrqapkgkglewvkvssggstyy 60
 |||||
 QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTVVYCARHNYGSFAYWGOGTTVTSS 117
 |||||
 Db 61 ldtvqgrftisrdnsnkntlylqmslraedtavvycarhnygsfaywgogttvtvss 117
 |||||

RESULT 3

AAW76003
 ID AAW76003 standard; Protein; 117 AA.

XX AAW76003;

XX 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

humanised antibody; antibody humanisation; antibody engineering
LM609; monoclonal antibody; complementarity determining region;
CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
cancer; therapy; diagnosis.

XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Sato K, Wakahara Y, Yabuta N;
 XX PS WPI; 1998-230640/20.
 XX DR
 XX CC New chimeric antibodies against human parathormone related
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 PT disorders caused by malignant neoplasm(s)
 XX PS Claim 21; Page 120; 182pp; Japanese.
 XX CC
 XX CC New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTHrP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphataemia such as that due to
 CC pathogens or to vitamin D resistance.
 XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 19; Length 118;
 Best Local Similarity 87.3%; Pred. No. 7.1e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
 Db 1 qvqlvesgggvqpgksrlrscasgftfssygmwvrqpgkglewatissggsytyy 60
 QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYICARHNYGS-FAYWGQGTITVTVSS 117
 Db 61 pdsvkgrftisrdsnknltlyqmnsrleadtavycarqtmtyfaywgggtltvtvss 118

RESULT 11
 AAW89636
 ID AAW89636 standard; Protein; 118 AA.
 XX AC AAW89636;
 XX DT 14-APR-1999 (first entry)
 XX DE Human antibody heavy chain mature protein.
 XX KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW Inhibitor; humanised.
 XX OS Homo sapiens.
 XX PN WO9851329-A1.
 XX PD 19-NOV-1998.
 XX PF 13-MAY-1998; 98WO-JP02116.
 XX PR 18-JUL-1997; 97JP-0194445.
 XX PR 15-MAY-1997; 97JP-0125505.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ishii K, Sato K, Tunenari T;
 XX PS WPI; 1999-070101/06.
 XX PT Inhibitors of binding of parathyroid hormone related peptide to its

PT receptor - useful for, e.g. treatment of cachexia arising from
 XX cancer or other diseases
 XX Example 4; Page 81; 125pp; Japanese.
 XX CC The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC cancer, thereby improving the quality of life of the patient. The
 CC present sequence represents a human antibody heavy chain from the
 CC present invention.
 XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 20; Length 118;
 Best Local Similarity 87.3%; Pred. No. 7.1e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLVWAKVSSGGSTYY 60
 Db 1 qvqlvesgggvqpgksrlrscasgftfssygmwvrqpgkglewatissggsytyy 60
 QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYICARHNYGS-FAYWGQGTITVTVSS 117
 Db 61 pdsvkgrftisrdsnknltlyqmnsrleadtavycarqtmtyfaywgggtltvtvss 118

RESULT 12
 AAY77512
 ID AAY77512 standard; Protein; 118 AA.
 XX AC AAY77512;
 XX DT 26-APR-2000 (first entry)
 XX DE Peptide seq ID No: 56.
 XX KW Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.
 XX OS Homo sapiens.
 XX PN WO200000219-A1.
 XX PD 06-JAN-2000.
 XX PF 25-JUN-1999; 99WO-JP03433.
 XX PR 26-JUN-1998; 98JP-0180143.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Sato K, Tsunenari T;
 XX PS WPI; 2000-117115/10.
 XX PT Treatment of hypercalcaemic crisis with a substance inhibiting binding
 PT of parathyroid hormone related peptide to its receptor -
 XX Example.4; Page 95-96; 120pp; Japanese.
 XX CC The invention relates to a method of treatment of hypercalcaemic crisis.
 CC A composition for the treatment of hypercalcaemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypercalcaemic crisis, such as that associated with
 CC a malignant tumour.

XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 21; Length 118;
 Best Local Similarity 87.3%; Pred. No. 7.le-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVRWQAPGKGLEWVAKVSGGGSTYY 60
 DB 1 qvqlvesgggvvqpgrsrlscaasgftfssygmwvrrqapkgglewvatisssggsytyy 60

QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYYCARHNYGS-FAYWGQGTVTVSS 117
 DB 61 pdsvkgrftisrdsnkntlylqmnsiraedtavyycarqgtmttyfaywggtlvtvss 118

RESULT 13
 AAB76890
 ID AAB76890 standard; Protein; 118 AA.
 AC AAB76890;
 DT 12-APR-2001 (first entry)
 DE Human antibody H chain Cregion C gamma 1 protein SEQ ID NO:56.
 KW Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin;
 KW monoclonal antibody; antidiarrheic; antileptic; antidiabetic;
 KW antipyretic; cancer; dehydration; excessive urination; thirst;
 KW vomiting; diarrhoea; fever; perspiration; diabetes.
 XX Homo sapiens.
 XX OS
 XX PN WO200102010-AL.
 XX PD 11-JAN-2001.
 XX PF 03-JUL-2000; 2000WO-JP04413.
 XX PR 02-JUL-1999; 99JP-0189322.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ogata E, Onuma E, Tsunenari T, Saito H, Azuma Y;
 XX WPI; 2001-112507/12.
 PT Inhibitor of parathyroid hormone related peptide binding to its
 PT receptor can ameliorate symptoms caused by a decrease in vasopressin
 PT level due to cancer -
 XX Example 2; Page 87-88; 114pp; Japanese.
 XX The present invention describes an agent (I) for ameliorating low
 CC vasopressin levels, and symptoms caused by this depression, containing
 CC as an active component a substance which inhibits the binding of
 CC parathyroid hormone related peptide (PTHrP) to its receptor. (I) has
 CC antidiarrheic, antileptic, antidiabetic and antipyretic activities.
 CC (I) can be used for the amelioration of symptoms caused by decrease in
 CC vasopressin levels, such as that due to cancer are treated using the
 CC agent. These symptoms include dehydration, excessive urination, thirst,
 CC vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to
 CC AAF69140 and AAB76879 to AAB76897 represent sequences used in the
 CC exemplification of the present invention.

XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 22; Length 118;
 Best Local Similarity 87.3%; Pred. No. 7.le-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVRWQAPGKGLEWVAKVSGGGSTYY 60
 DB 1 qvqlvesgggvvqpgrsrlscaasgftfssygmwvrrqapkgglewvatisssggsytyy 60

QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYYCARHNYGS-FAYWGQGTVTVSS 117
 DB 61 pdsvkgrftisrdsnkntlylqmnsiraedtavyycarqgtmttyfaywggtlvtvss 118

RESULT 14
 AAB76909
 ID AAB76909 standard; Protein; 118 AA.
 AC AAB76909;
 DT 17-APR-2001 (first entry)
 DE Human antibody H chain Cregion C gamma 1 protein SEQ ID NO:56.
 KW Human; mouse; hypercalcaemia; parathyroid hormone; PTH; PTHrP;
 KW parathyroid hormone related peptide; analgesic; immunosuppressive;
 KW nootropic; neuroprotective; antiinflammatory; cytostatic; antithyroid;
 KW eating-disorder; cardiovascular; pain; immune suppression; appetite;
 KW digestive system; protein metabolism; sugar metabolism; lipid metabolism;
 KW blood chemistry; thyroid function; electrolyte balance; neurological;
 KW central nervous system disorder; sleep disturbance; brain function;
 KW brain circulation; autonomic nervous system; blood poisoning; dropsy;
 KW inflammation; blood disease; calcium disturbance; autoimmune disease.
 XX Homo sapiens.
 XX OS
 XX PN WO200102011-AL.
 XX PD 11-JAN-2001.
 XX PF 03-JUL-2000; 2000WO-JP04414.
 XX PR 02-JUL-1999; 99JP-0189793.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ogata E, Sato K, Onuma E, Tsunenari T, Saito H, Azuma Y;
 XX WPI; 2001-123065/13.
 PT Agents modifying the binding of ligands to parathyroid hormone receptor
 PT or parathyroid hormone related peptide receptor for treatment of
 PT disorders associated with parathyroid hormone other than hypercalcaemia
 XX Example; Page 98-99; 130pp; Japanese.
 XX The present invention describes an agent (I) for the treatment and
 CC prevention of diseases other than hypercalcaemia associated with
 CC parathyroid hormone (PTH) or parathyroid hormone related peptide (PTHrP).
 CC (I) contains as an active component a substance which promotes or
 CC inhibits the binding of ligands to PTH receptor or PTHrP receptor, or is
 CC an agonist or antagonist to these receptors. (I) have analgesic,
 CC immunosuppressive, nootropic, neuroprotective, antiinflammatory,
 CC cytostatic, antithyroid, eating-disorders and cardiovascular activities.
 CC (I) is used for treatment and prevention of disorders associated with
 CC or PTHrP, including: pain; immune suppression; disturbances of the
 CC digestive system, protein metabolism, sugar metabolism, lipid metabolism,
 CC appetite, blood chemistry, thyroid function, and electrolyte balance;
 CC central nervous system disorders such as sleep disturbance, neurological
 CC disturbances, brain function disturbance, brain circulation disturbance
 CC and autonomic nervous system disturbance; and disorders caused by PTH or
 CC PTHrP associated cytokine cascade including blood poisoning, dropsy,
 CC inflammation, blood disease, calcium disturbance and autoimmune disease.
 CC Treatment and prevention of disorders other than hypercalcaemia which
 CC are associated with PTH or PTHrP, especially those associated with
 CC malignant tumours, and thereby ameliorating the quality of life of these
 CC patients. AAF69141 to AAF69196 and AAB76898 to AAB76916 represent

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OM protein - protein search, using sw model

Run on: October 11, 2001, 11:45:50 ; Search time 25.17 Seconds
(without alignments)
95.712 Million cell updates/sec

Title: US-08-791-391a-2

Perfect score: 616

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Scoring table: BLOSUM62

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Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 5: /cgn2_6/ptodata/2/1aa/PT05_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	517.5	84.0	139	1	US-08-129-930B-96
2	505	82.0	113	3	US-08-974-899-6
3	503.5	81.7	135	4	US-08-579-378A-20
4	503.5	81.7	443	5	PCT-US96-13152-4
5	502.5	81.6	122	2	US-07-934-373C-21
6	502.5	81.6	122	3	US-08-437-642B-21
7	502.5	81.6	122	5	PCT-US93-07832-21
8	502	81.5	119	1	US-08-053-171-12
9	502	81.5	125	1	US-08-478-039-99
10	502	81.5	125	1	US-08-476-349A-99
11	500.5	81.2	131	4	US-08-983-607-28
12	500	81.2	117	4	US-08-752-693A-4
13	497.5	80.8	122	5	PCT-US93-08435-12
14	497.5	80.8	122	5	PCT-US93-08435-43
15	496	80.5	119	1	US-07-988-925-11
16	496	80.5	119	2	US-08-362-780-11
17	495	80.4	119	1	US-08-331-398A-46
18	495	80.4	119	2	US-08-331-379B-46
19	495	80.4	119	2	US-08-759-804A-46
20	495	80.4	119	5	PCT-US94-07659-6
21	494.5	80.3	117	1	US-07-942-245-36
22	494.5	80.3	122	5	PCT-US93-08435-14
23	494	80.2	120	1	US-07-942-245-35
24	494	80.2	125	2	US-08-428-197-1
25	494	80.2	125	5	PCT-US93-10555-1
26	492.5	80.0	116	4	US-08-983-607-36
27	491	79.7	123	2	US-08-665-202-30

28	489.5	79.5	120	2	US-07-934-373C-4	Sequence 4, Appli
29	489.5	79.5	120	3	US-08-437-642B-4	Sequence 4, Appli
30	489	79.4	119	1	US-08-207-996-22	Sequence 22, Appl
31	489	79.4	119	2	US-08-760-840A-22	Sequence 22, Appl
32	489	79.4	119	3	US-09-266-119-22	Sequence 22, Appl
33	489	79.4	120	2	US-08-428-197-20	Sequence 20, Appl
34	489	79.4	120	5	PCT-US93-10555-20	Sequence 20, Appl
35	488.5	79.3	135	4	US-08-619-491-8	Sequence 8, Appli
36	487	79.1	117	2	US-08-652-558-44	Sequence 44, Appl
37	487	79.1	120	2	US-08-428-197-22	Sequence 22, Appl
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39	486	78.9	117	2	US-08-652-558-46	Sequence 46, Appl
40	486	78.9	117	4	US-08-983-607-46	Sequence 46, Appl
41	486	78.9	120	2	US-08-428-197-24	Sequence 24, Appl
42	486	78.9	120	2	US-08-428-197-26	Sequence 26, Appl
43	486	78.9	120	2	US-08-428-197-28	Sequence 28, Appl
44	486	78.9	120	5	PCT-US93-10555-24	Sequence 24, Appl
45	486	78.9	120	5	PCT-US93-10555-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRECC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-129-930B-96

Query Match 84.0%; Score 517.5; DB 1; Length 139;
Best Local Similarity 83.3%; Pred. No. 7.4e-46;
Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLVSGGTVQPGKSLRLSCLASGFTFSYDMSVWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQVSGGGLVQPGGSLRLSCLASGFAFSSYAMSVWVRQAPGKLEWAEISSGGNYAY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGS---FAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 QDVTGRTISRDNKNTLYLQMSLRADETAVYYCAREDYGIPAFWYWGQGTFTVSS 139

RESULT 2
US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899

FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear

US-08-974-899-6

Query Match 82.0%; Score 505; DB 3; Length 113;
Best Local Similarity 83.8%; Pred. No. 1.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLVSGGTVQPGKSLRLSCLASGFTFSYDMSVWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVSGGGLVQPGGSLRLSCLASGFTFSYAMSVWVRQAPGKLEWVVISGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGSFAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ADSVKGRTISRDNKNTLYLQMSLRADETAVYYCAR----GFYWGQGTFTVSS 113

RESULT 3
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A

FILING DATE: 27-DEC-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074

FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8

FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.

REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-579-378A-20

Query Match 81.7%; Score 503.5; DB 4; Length 135;
Best Local Similarity 83.8%; Pred. No. 1.9e-44;
Matches 98; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVSGGTVQPGKSLRLSCLASGFTFSYDMSVWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVSGGGLVQPGGSLRLSCLASGFTFSYAMSVWVRQAPGKLEWASIST-GGSTYY 78

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGSFAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 79 PDSVKGRTISRDNKNTLYLQMSLRADETAVYYCARDYDGYFYWGQGTFTVSS 135

RESULT 4
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson

STREET: 805 Third Avenue
CITY: New York

STATE: New York
COUNTRY: U.S.A.

```
;
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 81.7%; Score 503.5; DB 5; Length 443;
Best Local Similarity 83.8%; Pred. No. 7.7e-44;
Matches 98; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQVESGGVVQPGSRSLRSCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVASIST-GGSTYY 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 LDTVGRTISRDNKNTLYLQMSLRADTAVYYCARHNTGSAFYWGQGTIVTSS 117
Db 60 PDSVKGRTISRDNKNTLYLQMSLRADTAVYYCARDYDYGDFYWGQGTIVTSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
:1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/934,373C
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; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-21

Query Match 81.6%; Score 502.5; DB 2; Length 122;
Best Local Similarity 80.3%; Pred. No. 2.2e-44;
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

Qy 1 QVQVESGGVVQPGSRSLRSCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSVISDGGSTYY 60
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:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
:1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 LDTVGRTISRDNKNTLYLQMSLRADTAVYYCARHNY-----GSFAYWGQGTIVT 115
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAVYYCARGVGSLSGLDYWGQGTIVT 120
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:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
:1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 116 SS 117
Db 121 SS 122

RESULT 6
US-08-437-642B-21
; Sequence 21, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
```



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; ; * OTHER INFORMATION: /note= "Complementarity-determining
; ; OTHER INFORMATION: region"
; ; FEATURE:
; ; NAME/KEY: Region
; ; LOCATION: 50..66
; ; OTHER INFORMATION: /note= "Complementarity-determining
; ; OTHER INFORMATION: region"
; ; FEATURE:
; ; NAME/KEY: Region
; ; LOCATION: 99..108
; ; OTHER INFORMATION: /note= "Complementarity-determining
; ; OTHER INFORMATION: region"
US-08-053-171-12

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	Query Match	81.5%	Score 502;	DB 1;	Length 119;
	Best Local Similarity	81.5%;	Pred. No. 2.4e-44;		
	Matches 97;	Conservative 13;	Mismatches 7;	Indels 2;	Gaps 2;
Qy	1	QVLVESGGGVQGRSLRLSCAASGFTFSYDNMSVVRQAPGKGLVWAKVYSGGGSTYY	60		
		:			
Db	1	EVLLSEGGGLVQGGSLRLSCAASGFTFSYDYYWVVRQAPGKGLWVAYISNGGSSHY	60		
		:			
Qy	61	LDFVQGRFTISRNSKNTLYLQNNLSRAEDTAVYYCAR-HNYGS-FAYWGOGTTVTWSS	117		
		:			
Db	61	VDSVKGRFTISRNSKNTLYLQNNLSRAEDTALYICARGMDYGAWFAYWGOGTLVTWSS	119		
		:			

RESULT 9
 US-08-478-039-99
 ; Sequence 99, Application US/08478039
 ; Patent No. 5681722
 ; GENERAL INFORMATION:
 ; APPLICANT: Newman, Roland A.
 ; APPLICANT: Hanna, Nabil
 ; APPLICANT: Raab, Ronald W.
 ; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 ; NUMBER OF SEQUENCES: 114
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince St.
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,039
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/379,072
 ; FILING DATE: 25-JAN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/912,292
 ; FILING DATE: 10-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/856,281
 ; FILING DATE: 23-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/735,064
 ; FILING DATE: 25-JUL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin Esq., Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-160
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021

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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME: 18/2
; CHROMOSOME/SEGMENT: 18/2
; US-08-476-349A-99

Query Match 81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.5e-44;
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADETAVYYCARHN---YGFAY-----WGQGT 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGKGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGKQVLYYGGSYHWFDPWGQGT 120

QY 113 VTVSS 117
|||||
Db 121 VTVSS 125

RESULT 11
US-08-983-607-28
; Sequence 28, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983.607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V13
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-28

Query Match 81.2%; Score 500.5; DB 4; Length 131;
Best Local Similarity 82.1%; Pred. No. 3.7e-44;
Matches 96; Conservative 8; Mismatches 12; Indels 1; Gaps 1

QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGGLVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKGLWAKVSSGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGKQVLYYGGSYHWFDPWGQ 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGKGRFTISRDNKNTLYLQMSLRADETAVYYCARHNYGKQVLYYGGSYHWFDPWGQ 116

RESULT 12
US-08-752-693A-4
; Sequence 4, Application US/08752693A
; Patent No. 6190640
; GENERAL INFORMATION:
; APPLICANT: Sydney Welt
; APPLICANT: Gerd Ritter
; APPLICANT: Leonard Cohen
; APPLICANT: Clarence William Jr.
; APPLICANT: Elizabeth Carswell Richards
; APPLICANT: Mary John
; TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
; USING HUMANIZED ANTIBODIES WHICH
; BIND TO ANTIGEN A33
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PAULINE STASIAR, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.693A
; FILING DATE: 19-NO. 6190640-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07321
; FILING DATE: May 21, 1996
; APPLICATION NUMBER: 08/020,223
; FILING DATE: February 16, 1993
; APPLICATION NUMBER: 07/673,153
; FILING DATE: March 18, 1991
; APPLICATION NUMBER: 07/327,765
; FILING DATE: March 23, 1989
; APPLICATION NUMBER: 07/118,411
; FILING DATE: No. 6190640ember 6, 1987
; APPLICATION NUMBER: 06/724,991
; FILING DATE: April 19, 1985

```

ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 117
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: SEQ ID NO: 4
ORIGINAL SOURCE:
ORGANISM: Human A33
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-752-693A-4

Query Match 81.2%; Score 500; DB 4; Length 117;
Best Local Similarity 80.3%; Pred. No. 3.7e-44;
Matches 94; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
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DB 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWATISSGGSTYY 60
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QY 61 LDTVOGRTISRDNKNTLYLQMSLRADTAIVYCARHNTGSAFYWGQGTIVTVSS 117
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DB 61 LDSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAPTVVPFAYWGQGTIVTVSS 117
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RESULT 13

PCT-US93-08435-12
; Sequence 12, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: the Army
; APPLICANT: U. S. Government, Secretary of
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-43

Query Match 80.8%; Score 497.5; DB 5; Length 122;

SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-12

Query Match 80.8%; Score 497.5; DB 5; Length 122;
Best Local Similarity 79.5%; Pred. No. 7e-44; 11; Indels 5; Gaps 2;
Matches 97; Conservative 9; Mismatches 9;

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DB 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWSEISDGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVOGRTISRDNKNTLYLQMSLRADTAIVYCAR---HNYGSFA--YWGQGTIVTV 115
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QY 116 SS 117
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DB 121 SS 122
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RESULT 14

PCT-US93-08435-43
; Sequence 43, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-43

Query Match 80.8%; Score 497.5; DB 5; Length 122;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:29 ; Search time 2122.65 Seconds
(without alignments)
2339.127 Million cell updates/sec

Title: US-08-791-391A-3
Perfect score: 321
Sequence: 1 GAGATTGTGCTAACTCAGTC.....GGACCAAGTGGAATTAAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_ba2:*
3: gb_ba3:*
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5: gb_in2:*
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9: gb_pat1:*
10: gb_pat2:*
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12: gb_pl1:*
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14: gb_pl3:*
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22: em_htg_hum1:*
23: em_htg_hum2:*
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28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
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35: em_hum2:*
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37: em_hum4:*
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90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	321	100.0	321	9	AX060782 Sequence
2	318	99.1	321	9	AX060810 Sequence
3	268.2	83.6	321	9	AX060786 Sequence
4	249.6	77.8	321	94	MUSCMVF Mouse mRNA
5	249.6	77.8	321	94	MUSIGKAC Mouse Ig ac
6	249.6	77.8	370	94	MUSIGKXD AF163757 Mus muscu
7	248	77.3	321	94	AF163757 Mus muscu
8	248	77.3	321	94	MUSCMVF Mouse mRNA

9 248 77.3 381 10 E07933 cDNA encodi
10 248 77.3 381 10 I31959
11 248 77.3 381 10 I78571 Sequence 82
12 248 77.3 381 10 I78626 Sequence 82
13 248 77.3 381 10 I78626 Sequence 82
14 246.4 76.8 324 94 AF139844
15 246.4 76.8 324 94 AF139849
16 246.4 76.8 330 94 AF139849
17 246.4 76.8 324 94 AF139845
18 246.4 76.8 324 94 AF139845
19 244.8 76.3 324 94 AF139846
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21 244.8 76.3 324 94 AF139846
22 244.8 76.3 324 94 AF139846
23 243.2 75.8 321 94 AF139847
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25 243.2 75.8 321 94 AF139847
26 243.2 75.8 321 94 AF139847
27 243.2 75.8 321 94 AF139847
28 243.2 75.8 321 94 AF139847
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30 243.2 75.8 321 94 AF139847
31 241.6 75.3 324 94 AF139847
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34 241.6 75.3 324 94 AF139847
35 238.8 74.4 317 94 AF139847
36 237.4 74.0 313 94 AF139847
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ALIGNMENTS

RESULT 1
AX060782 321 bp DNA PAT 22-JAN-2001
LOCUS Sequence 3 from Patent WO0078815.
DEFINITION AX060782
ACCESSION AX060782
VERSION AX060782.1 GI:12406162
SOURCE synthetic construct.
ORGANISM synthetic construct.
KEYWORDS 1 (bases 1 to 321)
REFERENCE Huse,W.D. and Wu,H.
AUTHORS Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
TITLE encoding same and methods of use
JOURNAL Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
source 1..321
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/db_xref="taxon:32630"
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/translation="EIVTQSPATLSLSPGERATISCOASQISNHLHWYQORPQAP
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BASE COUNT 78 a 93 c 79 g 71 t
ORIGIN

Query Match 100.0%; Score 321; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.4e-90;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCCTCTCTCTCAGCCAGGAGAAAGGGGACT 60
Db 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCCTCTCTCTCAGCCAGGAGAAAGGGGACT 60
QY 61 CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
Db 61 CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCCGCC 180
Db 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCCGCC 180
QY 181 AGTTTCAGTGGCAGTGGATGAGGAGAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
Db 181 AGTTTCAGTGGCAGTGGATGAGGAGAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGG 300
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGG 300
QY 301 GGGACCAAGGTGGAATTAAG 321
Db 301 GGGACCAAGGTGGAATTAAG 321
RESULT 2
AX060810 321 bp DNA PAT 22-JAN-2001
LOCUS Sequence 31 from Patent WO0078815.
DEFINITION AX060810
ACCESSION AX060810
VERSION AX060810.1 GI:12406189
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL Patent: WO 0078815-A 31 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
source 1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="grafted antibody variable region"
variation 145..147
/note="NNN-CGT OR ATG"
BASE COUNT 76 a 93 c 78 g 71 t 3 others
ORIGIN

Query Match 99.1%; Score 318; DB 9; Length 321;
Best Local Similarity 99.1%; Pred. No. 4.8e-89;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCCTCTCTCTCAGCCAGGAGAAAGGGGACT 60
QY 61 CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
Db 61 CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCCGCC 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and
Brooks, W.B.R.
TITLE A three-dimensional model of an anti-lysozyme antibody
JOURNAL J. Mol. Biol. 194, 713-724 (1987)
MEDLINE 88011212
FEATURES
Source Location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/note="lysozyme binding Ig kappa chain V23-J2 region"
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BASE COUNT 88 a 80 c 75 g 78 t
ORIGIN

Query Match 77.8%; Score 249.6; DB 94; Length 321;
Best Local Similarity 86.2%; Pred. No. 1.4e-67;
Matches 276; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 GAGATTGCTACTCAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
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DB 1 GATATTGTCTACTCAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
QY 61 CTTCCTCGCAGGCCAGCAAGTATTAGCAACCACTACCTGCTATCAACAAGGCGCT 120
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DB 61 CTTCCTCGCAGGCCAGCAAGTATTAGCAACCACTACCTGCTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
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DB 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
QY 181 AGGTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCAGTATCCAGTCTGGAGCT 240
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DB 181 AGGTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCAGTATCCAGTCTGGAGCT 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTCAGTCCAGTCTGGAGGG 300
|||
DB 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTCAGTCCAGTCTGGAGGG 300
QY 301 GGGACCAAGGTGGAATATA 320
|||
DB 301 GGGACCAAGGTGGAATATA 320

RESULT 6
MUSIGKXD MUSTGKXD 370 bp mRNA ROD 27-APR-1993
LOCUS Mouse Ig active kappa-chain V-region, partial cds.
DEFINITION M93959
ACCESSION M93959
VERSION M93959.1 GI:197572
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 370)
AUTHORS Takeda, I., Wise, K.S. and Hoffman, R.W.
TITLE Nucleotide sequences of immunoglobulin heavy and light chain
V-regions from a monoclonal autoantibody specific for a unique set
of small nuclear ribonucleoprotein complexes
JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)
MEDLINE 92375706
FEATURES
Source Location/Qualifiers

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/db_xref="taxon:10090"
/map="6"
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BASE COUNT 96 a 90 c 86 g 98 t
ORIGIN

Query Match 77.8%; Score 249.6; DB 94; Length 370;
Best Local Similarity 86.2%; Pred. No. 1.4e-67;
Matches 276; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 GAGATTGCTACTCAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
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DB 37 GATATTGTCTACTCAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 96
QY 61 CTTCCTCGCAGGCCAGCAAGTATTAGCAACCACTACCTGCTATCAACAAGGCGCT 120
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DB 97 CTTCCTCGCAGGCCAGCAAGTATTAGCAACCACTACCTGCTATCAACAAGGCGCT 156
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
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DB 157 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 216
QY 181 AGGTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCAGTATCCAGTCTGGAGCT 240
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DB 217 AGGTCAGTGGCAGTGGATCAGGACAGATTTCACTCAGTATCAACAGTCTGGAGCT 276
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DB 277 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTAAACAGCTGGCGCTCATAGTTCGGATCG 336
QY 301 GGGACCAAGGTGGAATATA 320
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DB 337 GGGACCAAGGTGGAATATA 356

RESULT 7
AF163757 AF163757 321 bp mRNA ROD 04-AUG-1999
LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.
ACCESSION AF163757
VERSION AF163757.1 GI:5690320
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
Mouse Monoclonal Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Mertens, N.M. and Cunningham, M.W.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma


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Query Match      77.3%; Score 248; DB 10; Length 381;
Best Local Similarity 85.9%; Pred. No. 4.6e-67;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 61 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCCT 120
Db 121 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 180
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QY 181 AGGTTTTCAGTGGATGATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 240
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Db 361 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 360

RESULT 10
LOCUS      I31959      381 bp      DNA      PAT      06-FEB-1997
DEFINITION      Sequence 82 from patent US 5585089.
ACCESSION      I31959
VERSION      I31959.1 GI:1822750
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 381)
AUTHORS      Queen,C.L. and Selick,H.E.
TITLE      Humanized immunoglobulins
JOURNAL      Patent: US 5585089-A 82 17-DEC-1996;
FEATURES      Location/Qualifiers
             source
             1..381
             /organism="unknown"
BASE COUNT      97 a      92 c      89 g      103 t
ORIGIN

Query Match      77.3%; Score 248; DB 10; Length 381;
Best Local Similarity 85.9%; Pred. No. 4.6e-67;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGACT 60
Db 61 GATATTGTGCTACTCAGTCTCAGCCACCCCTGCTGTGACTCCAGGAGATAGCGTCACT 120
QY 61 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCCT 120
Db 121 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 240
QY 181 AGGTTTTCAGTGGATGATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 240
Db 301 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 360
QY 301 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 360
Db 361 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCATCTCTGGGATCCCGCC 360

RESULT 12
LOCUS      I78626      381 bp      DNA      PAT      03-APR-1998
DEFINITION      Sequence 82 from patent US 5693762.
ACCESSION      I78626
VERSION      I78626.1 GI:3014780
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 381)
AUTHORS      Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelingh,K.L.

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and Selick, H.E.
Humanized immunoglobulins
Patent: US 5693762-A 82 02-DEC-1997;
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RESULT 13
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LOCUS
DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN11K.
ACCESSION M19913 J03832
VERSION M19913.1 GI:157033
KEYWORDS C-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 56)
Rule,G.S.
Unpublished (1988)
AUTHORS 2 (bases 1 to 431)
Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
JOURNAL Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
REFERENCE Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
MEDLINE 88234486
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.
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RESULT 14
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LOCUS
DEFINITION Mus musculus clone 50 immunoglobulin kappa light chain variable
region Vx23 (IgG) mRNA, partial cds.
ACCESSION AF139844
VERSION AF139844.1 GI:4732152
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 324)
Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
Brard,F. and Weigert,M.
AUTHORS Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
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QY 181 AGGTTCAATGGCAGTGGATCAGGACAGATTTCACCTCAGTATCAACAGTGTGGAGCT 240
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QY 241 GAAGATTTTGGAGTGAATAA 320
Db 241 GGGACCAAGCTGGAATAA 320

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RESULT 15
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LOCUS
DEFINITION
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region Vk23 (Igg) mRNA, partial cds.
ACCESSION
AF139849
VERSION
AF139849.1 GI:4732162
KEYWORDS
house mouse.
SOURCE
Mus musculus.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 324)

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JOURNAL
MEDLINE
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REFERENCE
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JOURNAL
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Best Local Similarity 85.6%; Pred. No. 1.5e-66;
Matches 274; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCAGTCCAGCCACCCCTGCTCTCAGCCAGGAGGCGGCT 60
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QY 61 CTTTCCTCCAGCCAGCCAGGATATTAGCAACCACTACACTGCTATCAACAAAGGCT 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
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QY 181 AGGTTCAATGGCAGTGGATCAGGACAGATTTCACCTCAGTATCAACAGTGTGGAGCT 240
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QY 241 GAAGATTTTGGAGTGAATAA 320
Db 241 GGGACCAAGCTGGAATAA 320

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Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
99406777
10477553
2 (bases 1 to 324)
Brard,F. and Weigert,M.
Direct Submission
Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
Location/Qualifiers
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Job time: 6353 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:33:59 ; Search time 2341.88 Seconds
(without alignments)
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Perfect score: 321
Sequence: 1 GAGATTGCTAACTCAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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VERSION	BF579007.1	
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	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .	
AUTHORS	1 (bases 1 to 949)	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-r@mail.nih.gov	

SUMMARIES

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35	183.8	57.3	369	115	AW405943 UI-HF-BLO
36	183	57.0	833	172	BF975235 602244740
37	182.8	56.9	473	115	AW406934 UI-HF-BLO
38	182.2	56.8	518	115	AW406576 UI-HF-BLO
39	182.2	56.8	644	115	AW405817 UI-HF-BLO
40	182.2	56.8	719	154	BG536027 602564303
41	182	56.7	895	151	BF663197 602144313
42	181.2	56.4	1047	155	BG545346 602572793
43	180.8	56.3	425	115	AW406785 UI-HF-BLO
44	179	55.8	395	122	AW951626 EST363711
45	179	55.8	408	115	AW404674 UI-HF-BLO

ALIGNMENTS

RESULT 1
 BF582153
 LOCUS
 DEFINITION
 738 bp mRNA
 602099743F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4219402 5',
 EST
 BF582153
 mRNA sequence.
 BF582153.1 GI:11655865
 EST.
 house mouse.
 Mus musculus
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 738)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9792 row: p column: 05
High quality sequence start: 9
High quality sequence stop: 730.

FEATURES
source Location/Qualifiers

1. .949
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4216180"
/lab_host="NCLCGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCLCGAP Library."
BASE COUNT 278 a 241 c 210 g 220 t

Query Match 66.7%; Score 214; DB 150; Length 949;
Best Local Similarity 82.2%; Pred. No. 8.7e-56;
Matches 258; Conservative 0; Mismatches 55; Indels 1; Gaps 1;

QY 6 TGTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGGGACTCTTTTC 65
DB 83 TGTACTAACTCAGTCTCCAGCCACCTGCTGTGACTCTCCAGGAGATGCTGCTTTTC 142
QY 66 CTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCTGTGTCA 125
DB 143 CTGAGGCCAGCCAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCTGTGTCA 202
QY 126 AGCCCCAAGGCTTCTCATCAAGTATCTGTCCTCCAGTCCATCTCTGGATCCCGCCAGGTT 185
DB 203 GTCTCCGAGGCTTCTCATCAAGTTTGTTCCTCCAGTCCATCTCTGGATCCCGCCAGGTT 262
QY 186 CAGTGGCAGTGGATCAGGGACAGATTTTACCCTCACTATCTCCAGTCTCGAGGCTGAAGA 245
DB 263 CAGTGGCAGTGGATCAGGGACAAATTTTCACTCTCAGTATGCCCACTGTGGAGACTGAAGA 322
QY 246 TTTTGCAGTCTATCTGCTCAACAGAGTGGCAGCTGCCCTCACAGCTTCGGAGGGGGAC 305
DB 323 -TTTGAATGTATTTCTGTCCAGCAGATGACAGTTGGCCGGTCCACGTTCCGCTCCTGGGAC 381
QY 306 CAAGGTGGAAATTA 319
DB 382 CAACTGGAGCTGA 395

RESULT 3
BG569760 946 bp mRNA EST 10-APR-2001
LOCUS 602590367F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717049 5',
DEFINITION mRNA sequence.
ACCESSION BG569760
VERSION BG569760.1 GI:13577413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC <http://imgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgapps-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1566 row: e column: 18
High quality sequence stop: 738.

FEATURES
source Location/Qualifiers

1. .946
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4717049"
/lab_host="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGGCCGACATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 295 a 248 c 247 g 156 t

Query Match 64.3%; Score 206.4; DB 155; Length 946;
Best Local Similarity 77.8%; Pred. No. 2e-53;
Matches 249; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1 GAGATTGCTTAAGTCTCAGCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGCGACT 60
DB 96 GAAATCGTGTGACAGTCTCCAGCCACCTGCTCTTGTCTCCAGGAGAAAGGCGACC 155
QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 156 CTCTCCTCGAGGCCAGTCTCAGAGTGTAGCAGCCACTTAGCCTGGTACCAACAGAAACCT 215
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 216 GGCCAGGCTCCAGGCTCTCTATGATCATCAACAGGCGCCACTGGCATCGCAGCC 275
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCTCACTATCTCCAGTCTGGAGCCT 240
DB 276 AGTTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTTAGAGCCT 335
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
DB 336 GAAGATTTTGCAGTCTATTACTGTCTCAGCAGCTAGCACTGGCGCTCACTTTCGGCGGA 395
QY 301 GGGACCAAGGTGGAATTA 320
DB 396 GGGACCAAGGTGAGATTA 415

RESULT 4
AW406486 434 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BLO-acr-f-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060238 5', mRNA sequence.
ACCESSION AW406486
VERSION AW406486.1 GI:6925543
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 434)
NIH-MGC <http://imgc.nci.nih.gov/>.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 624)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Invitro Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8561 row: g column: 20
High quality sequence stop: 598.

FEATURES
source

1..624
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J (f1er1)"
/db_xref="taxon:10090"
/clone="IMAGE:3501355"
/clone_lib="NCI CGAP Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT
ORIGIN

172 a 166 c 145 g 141 t
Query Match 62.8%; Score 201.6; DB 166; Length 624;
Best Local Similarity 76.9%; Pred. No. 5.5e-52;
Matches 246; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACACAGTCTCCAGCCACCCGTCTCTCAGCCAGGAGGAGGCGACT 60
DB 59 GACATCTTGATGACCCAGTCTCCAGCCACCCGTCTGTGACTCCAGGAGAACAGTCACT 118
QY 61 CTTTCTGCGAGCCAGCCAGCAAGTATTAGCAACACCTACACTGCTGTATCAACAAGGCGCT 120
DB 119 CTTTCTGCTAGGCGCCAGCCAGCAATATTACAAAGAACCTACACTGCTGTATCAACAAGAAATCA 178
QY 121 GGTCAAGCCCAAGGCTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCGCC 180
DB 179 CATGGACTCCAGGCTCTCATCAAGTATGCACCTGATCCCATCTCTGGATCCCGCTCC 238
QY 181 AGGTTCAGTGGCAGTGGATCAGGACAGATTTTCACCCCTCACCTATCTCCAGTCTGGAGCCT 240
DB 239 AGTTCAGTGGCAGTGGATCAGGACAGATTTACATCTCAGTATCAACAGTGTGAAGCT 298
QY 241 GAAGATTTGAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGGG 300
DB 299 GAAGATGAAGGAATATTACTGTCTTCAAGGTTACAGCATGCCGTATACGTTCCGATCG 358
QY 301 GGGACCAAGTGGAAATTA 320
DB 359 GGGACCAAGCTGGAAATAA 378

RESULT 9
AW405025

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW405025 385 bp mRNA EST 16-FEB-2000
UI-HF-BL0-abx-e-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058252 5', mRNA sequence.
AW405025
AW405025.1 GI:6924082
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 385)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

1..385
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058252"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 88 a 114 c 98 g 85 t
ORIGIN

Query Match 62.7%; Score 201.2; DB 115; Length 385;
Best Local Similarity 77.0%; Pred. No. 6.3e-52;
Matches 245; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 3 GATTGTGCTAACTCAGTCTCCAGCCACCCGTCTCTCAGCCAGGAGGAGGCGACTCT 62
DB 7 GATTGTGTTGACACAGTCTCCAGCCACCCGTCTTTTGTCTCCAGGGGAAAGACCCCT 66
QY 63 TTCTGCCAGCCAGCCAGCAAGTATTAGCAACACCCCTACACTGTGTATCAACAAGGCGCT 122
DB 67 CTCTGTCAGGCGCAGTCAAGTGTTCGAGCTACTTAGCTGTGTACCAACAGAACTGG 126
QY 123 TCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGATCCCGCCAG 182
DB 127 CCAGGCTCCAGGCTCTCATCTATGATCATCAACAGGCGCACTGGCATCCAGCCAG 186
QY 183 GTTCAGTGGCAGTGGATCAGGACAGATTTTCACCCCTCACTATCTCCAGTCTGGAGCCTGA 242
DB 187 GTTCAGTGGCAGTGGGCTCTGGGACAGACTTCTCTCACCATCAGCAGCTAGAGCCTGA 246
QY 243 AGATTTTGAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGGGG 302
DB 247 AGATTTTGAGTCTATTACTGTGTCAGCGAAGCGACTGGCTCGGACGCTTGGCCAAAG 306
QY 303 GACCAAGGTGGAAATTA 320
DB 307 GACGAAGGTGGAAATCAA 324

RESULT 10
AW405643

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AW405643 468 bp mRNA EST 16-FEB-2000
UI-HF-BL0-abs-f-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057561 5', mRNA sequence.
AW405643
AW405643.1 GI:6924700
EST.
human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
1..468
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057561"
/tissue_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7f3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 110 a 137 c 115 g 106 t
ORIGIN

Query Match 62.3%; Score 200; DB 115; Length 468;
Best Local Similarity 76.6%; Pred. No. 1.6e-51;
Matches 245; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 1 GAGATTGTGTAAGTCTCCAGCCACCTGTCTCAGCCAGGAGAAAGGCGACT 60
Db 23 GAAATTTGTTGACACAGTCTCCAGCCACCTGTCTTGTCTCCAGGGGAAAGGCCAC 82
QY 61 CTTTCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCT 120
Db 83 CTCCTCGCAGGGCCAGTCAGAGTGTAGCGCTACTTAGCCTGGTACCAACAGACCT 142
QY 121 GGTCAAGCCCAAGGCTTCATCAAGTATGTTCCAGTCCCATCTCTGGGATCCCGGCC 180
Db 143 GGCAGGCTCCAGGCTCCATCATGTATGATGATCAACAGGGCCACTGGCATCCAGCC 202
QY 181 AGGTTTCAGTGGCAGTGGAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240
Db 203 AGGTTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACATCAGCAGCTAGAGCCT 262
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTACAGCTTCGGAGGG 300
Db 263 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTACCTTTCGGCCCT 322
QY 301 GGGACCAAGTGGAAATTA 320
Db 323 GGGACCAAGTGGATCA 342

RESULT 11

AW404506 468 bp mRNA EST 16-FEB-2000
LOCUS
DEFINITION UI-HF-BLO-aby-a-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058065 5', mRNA sequence.
ACCESSION AW404506
VERSION AW404506.1 GI:6923563

KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
1..468
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058065"
/tissue_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7f3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 106 a 137 c 114 g 111 t
ORIGIN

Query Match 61.8%; Score 198.4; DB 115; Length 468;
Best Local Similarity 76.2%; Pred. No. 5e-51;
Matches 244; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 1 GAGATTGTGTAAGTCTCCAGCCACCTGTCTCAGCCAGGAGAAAGGCGACT 60
Db 41 GAAATTTGTTGACACAGTCTCCAGCCACCTGTCTTGTCTCCAGGGGAAAGGCCAC 100
QY 61 CTTTCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCT 120
Db 101 CTCCTCGCAGGGCCAGTCAGAGTGTAGCAGCTTAGCCTGGTACCAACAGAAACCT 160
QY 121 GGTCAAGCCCAAGGCTTCATCAAGTATGTTCCAGTCCCATCTCTGGGATCCCGGCC 180
Db 161 GGCAGGCTCCAGGCTCCATCATGTATGATGATCAACAGGGCCACTGGCATCCAGCC 220
QY 181 AGGTTTCAGTGGCAGTGGAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240
Db 221 AGGTTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACATCAGCAGCTAGAGCCT 280
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTACAGCTTCGGAGGG 300
Db 281 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTACAGCTTCGGAGGG 340
QY 301 GGGACCAAGTGGAAATTA 320
Db 341 GGGACCAAGTGGAGATCA 360

RESULT 12

BG536848
LOCUS
DEFINITION BG536848 1015 bp mRNA EST 03-APR-2001
IMAGE:602566386F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691085 5',
mRNA sequence.


```
RESULT 14
BG568486      548 bp      mRNA      EST      10-APR-2001
LOCUS        602587455F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716468 5',
DEFINITION   mRNA sequence.
ACCESSION    BG568486
VERSION      BG568486.1 GI:13576139
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 548)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cyapbs-remail.nih.gov
              Tissue Procurement: CLONETECH Laboratories, Inc.
              cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LICM1564 row: m column: 13
              High quality sequence stop: 548.
              Location/Qualifiers
                location: 1..548
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4716468"
                /clone_lib="NIH_MGC_76"
                /lab_host="DH10B (TI phage-resistant)"
                /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
              SfiI (ggccgctcggcc); Site_2: SfiI (ggccattggcc); 5' and
              3' adaptors were used in cloning as follows: 5' adaptor
              sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:
              5'-ATTCTAGAGCCGAGCGGCACATG-dt(30)BN-3' (where B = A,
              C, G and N = A, C, G, or T). Average insert size 1.85
              kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
              by PCR. This library was enriched for full-length clones
              and was constructed by Clontech Laboratories (Palo Alto,
              CA). Note: this is a NIH_MGC Library."
BASE COUNT   126 a 162 c 139 g 121 t
ORIGIN
Query Match      61.0%; Score 195.8; DB 155; Length 548;
Best Local Similarity 75.9%; Pred. No. 3.4e-50;
Matches 242; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 GAGATTGTGTAAGTCTCAGCCAGCCCTGTCTCTCAGCCAGGAGGAGGCGCACT 60
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 106 GAAATTTGTTGACAGAGTCTCCAGCCAGCCCTGTCTTGTCTCAGGGGAAACAGCACC 165
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACCACTACATCGTATCAACAAGGCT 120
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 166 CTCTCTCGCAGGGCCAGTATGTTGGCAGCTACTTACGCTGGTACCAACAGAACT 225
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 121 GGTCACAGCCCAAGGCTTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCGCC 180
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 226 GGCCAGGCTCCAGGCTCCTCATCTATGATAGTCCACAGGCGCACTGGCGTCCAGCC 285
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 181 AGGTTACAGTCAGTGTGATCAGGACAGATTTACCTCTACTATCTCCAGCTGGAGCCT 240
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 286 AGGTTACAGTCAGTGTGATCAGGACAGATTTACCTCTACTATCTCCAGCTGGAGCCT 345
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTTCACAGCTTCGGAGGG 300
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 346 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTTCACAGCTTCGGAGGG 405
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 301 GGGACCAAGGTGGAAATTA 320
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 392 GGGACCAAGGTGGAGCTCAA 411
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 301 GGGACCAAGGTGGAAATTA 319
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 406 GGGACCAAGGTGGAAATCA 424
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 15
AV734882      485 bp      mRNA      EST      17-OCT-2000
LOCUS        AV734882 cda Homo sapiens cDNA clone cdABFC04 5', mRNA sequence.
DEFINITION    AV734882
ACCESSION     AV734882
VERSION       AV734882.1 GI:10852427
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 485)
AUTHORS       Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
              Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
              W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
              Chen,Z. and Han,Z.
TITLE         Homo sapiens cda cda clones
JOURNAL       Unpublished (2000)
COMMENT       Contact: Zequang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex.45)
              Fax: 86-21-50801922
              Email: hanzg@hgc.sh.cn
              This clone is available at CHGC in Shanghai.
              Location/Qualifiers
                location: 1..485
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="cdABFC04"
                /clone_lib="cda"
                /tissue_type="pheochromocytoma"
                /dev_stage="Adult"
                /lab_host="BM25.8"
                /note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI"
BASE COUNT   99 a 148 c 118 g 120 t
ORIGIN
Query Match      60.3%; Score 193.6; DB 110; Length 485;
Best Local Similarity 75.3%; Pred. No. 1.6e-49;
Matches 241; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 GAGATTGTGTAAGTCTCAGTCCTCCAGCCAGCCCTGTCTCTCAGCCAGGAGGAGGCGCACT 60
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 92 GAAATTTGTTGACAGAGTCTCCAGCCAGCCCTGTCTTGTCTCCAGGGGAAAGAGCCACC 151
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACCACTACATCGTATCAACAAGGCT 120
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 152 CTTTCCTGCCAGGCGCAGTGTAGAGTGTGTAGAGTCTCTAGCCCTGGTACCAACAGAAACCT 211
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 121 GGTCACAGCCCAAGGCTTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCGCC 180
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 212 GGCCAGGCTCCAGGCTCCTCATCTCTGATGATCCCAACAGGCGCCCTGGCATCCCAACC 271
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 181 AGGTTACAGTCAGTGTGATCAGGACAGATTTACCTCTACTATCTCCAGCTGGAGCCT 240
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 272 AGGTTAATGGCAGTGGTCTGGACAGAGTTCACCTCTCACCATTACAGCTTAAGAGCCT 331
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 241 GAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTTCACAGCTTCGGAGGG 300
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 332 GAGATTTCAGTCTATTACTGTCAACAGAGTGGCTGGCTTAACTTTTCGGCGGA 391
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY 301 GGGACCAAGGTGGAAATTA 320
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 392 GGGACCAAGGTGGAGCTCAA 411
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Search completed: October 11, 2001, 14:34:02
Job time: 5539 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:35 ; Search time 177.65 seconds
(without alignments)
1134.570 Million cell updates/sec

Title: US-08-791-391a-3

Perfect score: 321

Sequence: 1 GAGATTGTGCTACTCAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	19 AAV49821	Vitaxin antibody 1
2	321	100.0	321	22 AAF28176	Vitaxin light chain
3	318.6	99.3	321	19 AAV49843	LM609 antibody lig
4	318	99.1	321	22 AAF28199	DNA encoding light
5	268.2	83.6	321	19 AAV49823	LM609 antibody lig
6	268.2	83.6	321	22 AAF28178	Antibody LM609 lig
7	260.8	81.2	381	21 AA235244	Humanised anti-ver
8	252.8	78.8	321	20 AAV71800	Humanised anti-alp
9	252.8	78.8	338	20 AAV71802	Vitronectin alpha
10	248	77.3	381	15 AAQ64167	Sequence of mouse
11	248	77.3	381	22 AAF58747	Murine CMV5 antibo

12	241.6	75.3	324	20	AAV71798	Murine vitronectin
13	241.6	75.3	5238	11	AAQ04654	Plasmid pBT111 enc
14	235.2	73.3	381	21	AAZ35242	Mouse anti-verotox
15	233.6	72.8	651	21	AAA44346	Human secreted exp
16	232	72.3	416	18	AAAT49345	cDNA encoding kapp
17	230.4	71.8	324	17	AAAT33446	EGF receptor chime
18	230.4	71.8	415	21	AAAD0904	Humanised antibody
19	230.4	71.8	415	21	AAAD0906	Humanised antibody
20	225.6	70.3	8858	20	AAZ10202	Expression vector
21	224	69.8	363	17	AAZ38510	Light chain coding
22	224	69.8	486	14	AAQ43245	hIL2R Ab L chain v
23	220.8	68.8	415	21	AAQ01262	Mouse monoclonal a
24	219	68.2	315	20	AAV71803	Jk gene segment.
25	219	68.2	315	20	AAV71805	Humanised anti-alp
26	216	67.3	322	15	AAQ44714	Light chain variab
27	216	67.3	322	20	AAZ28545	Light chain variab
28	214.4	66.8	321	20	AAZ10203	DNA encoding the v
29	209.6	65.3	321	20	AAZ10205	DNA encoding the v
30	208	64.8	322	14	AAQ36615	Anti-IL2R-beta ant
31	208	64.8	1395	10	AAAN90300	Insert coding for
32	206.4	64.3	321	14	AAQ43243	B-B10 MAb L chain
33	206.4	64.3	321	19	AAV26766	Anti-gp54 MAb 48-1
34	206.4	64.3	324	22	AAZ29505	Human Fab clone LD
35	206.4	64.3	486	14	AAQ43384	L-chain V-region o
36	204.8	63.8	321	21	AAA40203	H. pylori beta-ure
37	204.8	63.8	381	18	AAAT49338	cDNA encoding kapp
38	204.8	63.8	416	18	AAAT49344	cDNA encoding kapp
39	204.8	63.8	416	18	AAAT49342	cDNA encoding kapp
40	203.4	63.4	318	14	AAQ48766	Monoclonal antibod
41	203.2	63.3	381	19	AAV12262	Monoclonal antibod
42	203.2	63.3	642	20	AAZ77408	Anti-human TNF-alp
43	202.2	63.0	720	19	AAV26770	Anti-gp54 MAb 48-1
44	201.6	62.8	794	17	AAAT42033	Plasmid pMW152-225
45	201.6	62.8	2070	17	AAAT42035	Plasmid pSW202-225

ALIGNMENTS

RESULT 1	
AAV49821	
ID	AAV49821 standard; DNA; 321 BP.
AC	AAV49821;
XX	
XX	
DT	02-NOV-1998 (first entry)
XX	
DE	Vitaxin antibody light chain variable region DNA.
XX	
KW	Vitaxin; antibody; variable region; heavy chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW	macular degeneration; osteoporosis; ss.
XX	
OS	Mus sp.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..321
FT	/product= a
FT	/tag=
FT	/note= "vitaxin antibody light chain variable region"
FT	/note= "partial sequence, no start or stop codon given"
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PN	WO9833919-A2.
XX	
PD	06-AUG-1998.
XX	
PF	30-JAN-1998; 98WO-US01826.
XX	
PR	30-JAN-1997; 97US-0791391.
XX	
PA	(IXSY-) IXSYS INC.
XX	

Glaser SM, Huse WD;
WPI: 1998-437472/37.
P-PSDB; AAW76002.

Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

Claim 6; Fig 1b; 129pp; English.

This sequence encodes the vitaxin antibody variable light chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 100.0%; Score 321; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGGACT 60
|||||
1 gagattgtgctaactcagttctcagccaccctgtctctcagccaggaagaaggcgact 60
|||||

61 CTTTCTGCGCAGGCCAGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCGT 120
61 ctttctgccagggccagccaaagtattagcaaccacctacactggtatccaacaaaggcct 120
|||||

121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
121 ggtcaagccccaaggcttctcataagtatcgttccagtcctcctctcggagtccccgcct 180
|||||

181 AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTACCTCACTATCTCCAGTCTGGAGCGT 240
181 aggttcagtggcagtggtatcagggaacagattccacctcactatctccagctggagcct 240
|||||

241 GAGATTTCAGTCTATTACTGTCACACAGTGGCAGTGGCCTCAACCGTTCGAGGG 300
241 gagattttcagtcctattactgtccaacagtggtggcagctggcctcacagcttcggagg 300
|||||

301 GGGACCAAGGTGGAAATTAAG 321
301 gggaccaagtggaataag 321
|||||

RESULT 2
AAF28176
ID AAF28176 standard; DNA; 321 BP.
XX AAF28176;
XX
DT 03-APR-2001 (first entry)
XX
XX Vitaxin light chain variable region DNA.
XX
XX LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
XX Unidentified.
XX
XX WO200078815-Al.
XX

Db 121 ggtcaagcccaaggcttctcatcnnntatcgttccagtcctatctctgtggatccccgcc 180
 QY 181 AGGTTCAAGTGGCAGTGCAGGACAGATTTCACCTCCTCACTATCTCCAGTCTGGAGCCT 240
 Db 181 aggttcagtggtgagtcagggacagattccaccctcactatctccagctcggagcct 240
 QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGCTTCGGAGGG 300
 Db 241 gaagatttgcagtcattactgtcaacagagtggcagctggcctcacacgttcggagg 300
 QY 301 GGGACCAAGTGGAAATTAAG 321
 Db 301 gggaccaagtggaattaa 321

RESULT 5
 AAV49823 standard; DNA; 321 BP.
 XX
 AC AAV49823;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 antibody light chain variable region DNA fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; ss.

XX Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..321
 FT /tag= a
 FT /product= "LM609 antibody light chain variable region"
 FT /note= "partial sequence, no start or stop codon given"
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 XX (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 XX WPI; 1998-437472/37.
 DR P-PSDB; AAW75004.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 40; Fig 2b; 129pp; English.

XX This sequence encodes the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.

SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
 Query Match 83.6%; Score: 268.2; DB 19; Length 321;
 Best Local Similarity 89.7%; Pred. No. 4.8e-75;
 Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
 Db 1 gatatgtgttaactcagtcctccagccaccctgtctgtgacaccaggagatagcgtcagt 60
 QY 61 CTTTCTGCTCCAGGCCAGCCAAAGTATTAGCAACACCTACTACTGGTATCAACAAGGCCT 120
 Db 61 cttctctgccaggccagccaaagtattagcaaccacacctacactggtatcaacaaaatca 120
 QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCTGTTCCAGTCCATCTCTGGATCCCCGCC 180
 Db 121 catgagctctccaggcttctcatcaagtatcgttccagttccatctctggatccccctcc 180
 QY 181 AGGTTCAAGTGGCAGTGGATCAGGACAGATTTCACCTCCTCACTATCTCCAGTCTGGAGCCT 240
 Db 181 aggttcagtggtgagtcagggacagatttctcagtcctcagtatcaacagtggtggagact 240
 QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGCTTCGGAGGG 300
 Db 241 gaagatttggaaatgtatttctgtcaacagagtggtcagctggcctcacacgttcggagg 300
 QY 301 GGGACCAAGTGGAAATTAAG 321
 Db 301 gggaccaagctggaaattaa 321

RESULT 6
 AAF28178 standard; DNA; 321 BP.
 XX
 ID AAF28178
 AC AAF28178;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Antibody LM609 light chain variable region DNA.
 XX
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 2; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

Query Match	83.6%	Score	268.2	DB	22	Length	321
Best Local Similarity	89.7%	Pred. No.	4.8e-75				
Matches	288	Conservative	0	Mismatches	33	Indels	0
Gaps	0						

QY	1	GAGATTGGCTAACTCAGCTCTCCAGCCACCCTGTCTCTCAGCCCGAGGAAAGGGCGACT	60
Db	1	gatattgtcaactcagctccagccaccctgtctgtgacaccaggagatagcgtcagt	60
QY	61	CTTTCTCTCCAGGCGCAGCAAGATTATTAGCAACCACTTACACTGGTATCAACAAAGGCGCT	120
Db	61	ctttctctgcagccagccaaagtatttagcaaccactacactggtatcaacaaaaatca	120
QY	121	GGTCAAGCCCCAAGCGTTCCTCATCAAGTATCGTTGCCAGTCCATCTCTGGGATCCCCGCC	180
Db	121	catgagctccaaagcttctcatcaagtatcgttcccagtcacatctctgggataccctcc	180
QY	181	AGGTTCAAGTGGCAGTGGATCAGGACAGATTTACCCCTCATTCTCCAGTCTGGAGCCT	240
Db	181	aggttcagtggcagtgagatcagggacagattcgtctcagtatcaacagttgtagagact	240
QY	241	GAAGATTTTGCAGTCTATTACTGTCAACACAGAGTGGCAGCTGGCCCTCACACGTTTCGGAGGG	300
Db	241	gaagatttggaaagtatttctgtcaacagagtggcagctggctccacagttctcgagagg	300
QY	301	GGGACCAAGGTGGAAATTAAG	321
Db	301	gggaccaagctggaaattaaq	321

RESULT	7	
AAZ35244		
ID	AAZ35244	standard; cDNA; 381 BP.
XX	XX	
XX	AC	AAZ35244;
XX	XX	
XX	DF	13-MAR-2000 (first entry)
XX	XX	
DE	XX	Humanised anti-verotoxin II antibody VTml-1 VL cDNA.
XX	XX	
KW	KW	Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW	KW	monoclonal antibody; light chain; mouse; human; humanised antibody;;
KW	KW	Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW	KW	HUS; therapy; ss.
XX	XX	
OS	OS	Homo sapiens.
OS	OS	Synthetic.

Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
WPI: 2000-086580/07.
P-PSDB: AAY32407.
Humanized antibody binding to verotoxin II used for treating Verotoxin
producing E. coli -
Disclosure; Fig 2b; 59pp; English.
This DNA sequence codes for a humanised light chain variable region
(see AAY32407) of murine monoclonal antibody Vtm1-1 (MuVtm1-1), an
antibody that specifically binds to the B subunit of verotoxin II
(VT2). The invention relates to humanised antibodies against VT2
that are capable of neutralizing VT2 and/or VT2 variants. The
humanised antibody is a humanized form of MuVtm1-1 comprising the
complementarity determining regions of MuVtm1-1 (see AAY32404-05) and
heavy and light chain variable region frameworks from the human GF4
antibody heavy and light chain frameworks, provided that at least 1
position selected from L49, H29, H30, H49 and H98 is occupied by the
amino acid at the equivalent position of the MuVtm1-1 antibody heavy
or light chain variable region framework. Such humanized antibodies
have an affinity for VT2 that is 3-, 5 or 10-times that of MuVtm1-1.
They are used for treating a patient suffering from, or at risk of,
the toxic effects from VT2 (claimed), especially for treating
verotoxin producing *Escherichia coli* (VTEC) infection, and haemolytic
uraemic syndrome (HUS).
Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match	81.2%;	Score 260.8;	DB 21;	Length 381;
Best Local Similarity	88.4%;	Pred. No. 1.1e-72;		
Matches 283;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;

Qy	1	GAGATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCGAGGAGAAAGGCGAGCT	60
Db	61	gaaattgctcaactcagctcccgccaccctgtctgtctccaggagaagagccact	120
Qy	61	CTTTCTCTGCCAGGCCAGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCCT	120
Db	121	ctttctcagggccagtcacactattagcaaacctcacatggtatcaacaaaacca	180
Qy	121	GGTCAAGCCCCAAGGCTTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGATCCCGGCC	180
Db	181	ggtcaggctccaaagctctctcatcaagctgtctcccgatcatctctggatccccccc	240
Qy	181	AGGTTCACTGGCAGTGGATCAGGGACAGATTTCACCCCTCAGTCTCCAGTCTGGAGCCT	240
Db	241	aggttcagtgccagtggaatcaggagacagatttcactctcactatcagcagctcggaaatct	300
Qy	241	GAGATTTTGTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTTCACACGTTCGGAGGG	300
Db	301	gaagatttgcagtgattactgtcaacagaggttacagctggcgctcacgttcoggtcaca	360
Qy	301	GGGACCAAGGTGGAAATTAA	320
Db	361	gggaccaaggtggagatcaa	380

RESULT	8
AAV71800	
ID	AAV71800 standard; cDNA; 321 BP.
XX	AC
XX	AAV71800;
XX	
XX	
XX	15-MAR-1999 (first entry)
XX	
XX	Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL cDNA.
XX	
KW	Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW	mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

PA (TEIJ) TEIJIN LTD.
PA (PROT-) PROTEIN DESIGN LABS INC

Db 1 gacatagtagtactgactcagctccaggccaccctgtcttctccaggagaaagagccacc 60
QY 61 CTTTCTCCAGGCCAGCAAGATATTAGCACACCTACACTGCTATCAACAAGGCT 120
Db 61 cttctctcaggccagcgaagattagcaaccctcacactggtatcaacaacaacct 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180
Db 121 ggcaggctcgcggcttctcatcaagtagcttcccaagtcattctgggattccctcc 180
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Db 181 aggttcagtgagtgagtcagggacagatttccactctcaccatcagcgtctagagct 240
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Db 241 gaagattttgcggtttattactgtcaacagagataaacagctggccttcacgctcgccag 300
QY 301 GGGACCAAGGTGGAAATTA 320
Db 301 ggtaccaaggtggaataaa 320

RESULT 10

AAQ64167
ID AAQ64167 standard; cDNA to mRNA; 381 BP.

AC AAQ64167;

DT 29-DEC-1994 (first entry)

XX Sequence of mouse V-kappa showing the sequences of recombinant
DE anti-FHV-1 antibody CDRs 1, 2 and 3.

XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW complementarity determining region; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 1..381

FT /*tag= a

FT misc_feature 19

FT /*tag= b

FT /label= MKL104

FT 385..429

FT /*tag= C

FT /label= MKL124

XX WO9412661-A.

XX 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.

XX 28-NOV-1992; 92JP-0341255.

XX (KAGA) CHERO SERO THERAPEUTIC RES INST.

XX Kinachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX WPI; 1994-200288/24.

XX P-PSDB; AAR54093.

XX Feline monoclonal antibody and recombinant antibodies specific

XX for FHV-1 - for detection, treatment and prevention of FHV-1

XX infection.

XX Disclosure; Page 18-19; 53pp; Japanese.

XX The inventors claim a monoclonal antibody against feline herpes

XX virus (FHV-1). They also claim a recombinant antibody against FHV-1

CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
CC used in the detection, treatment and prevention of FHV-1. The
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
CC antibody are given in AAR54092. The sequences of the CDRs in the VL of
CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR
CC sequences are claimed.

XX Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;

Query Match 77.3%; Score 248; DB 15; Length 381;
Best Local Similarity 85.9%; Pred. NO. 1.2e-68;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60

Db 61 gatatgtgctaaactcagctctccagccacctgtctgtgactcccgagagatagctcagt 120

QY 61 CTTTCTCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGCTATCAACAAGGCT 120

Db 121 cttctctcaggccagcgaagattagcaacaacctcacactggtatcaacaacaacct 180

QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180

Db 181 catgagttcccaaggcttctcatcaagtagtctccagtcattctctgggattccctcc 240

QY 181 AGGTTCACTGGCAGTGGATGAGGACAGATTCACCTCACATCTCCAGTCTGGAGCT 240

Db 241 aggttcagtgagtgagtcagggacagatttccactctcaccatcagcgtctagagct 300

QY 241 GAAGATTTTGAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGG 300

Db 301 gaagattttgcggtttattactgtcaacagagataaacagctggccttcacgctcgccag 360

QY 301 GGGACCAAGGTGGAAATTA 320

Db 361 gggaccaagctggagctgaa 380

RESULT 11

AAF58747
ID AAF58747 standard; cDNA; 381 BP.

AC AAF58747;

DT 30-APR-2001 (first entry)

XX Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;
KW ss.

XX Mus sp.

XX US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX DR

Qy	301	GGGACCAAGGTGGAAATTAA	320
Db	307	gggaccaagctggagctgaa	326
RESULT 14			
AAZ35242			
ID	AAZ35242	standard; cDNA; 381 BP.	
XX	AC		
XX	AAZ35242;		
XX	13-MAR-2000	(first entry)	
XX	Mouse anti-verotoxin II antibody VTml-1 VL cDNA.		
XX	Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;		
KW	monoclonal antibody; light chain; mouse; humanised antibody;		
KW	Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;		
KW	HUS; therapy; ss.		
XX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	sig_peptide	1..60	
FT		/*tag= a	
FT	mat_peptide	58..381	
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FT		/transl_except= (pos:184..186, aa:Lys)	
XX			
XX	WO9959629-A1.		
XX			
PD	25-NOV-1999.		
XX			
PF	19-MAY-1999;	99WO-US11179.	
XX			
PR	20-MAY-1998;	98US-0086570.	
XX			
PA	(TEIJ) TELJIN LTD.		
PA	(PROT-) PROTEIN DESIGN LABS INC.		
XX			
PI	Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;		
XX			
DR	WPI; 2000-086580/07.		
DR	P-PSDB; AAY32405.		
XX			
PT	Humanized antibody binding to verotoxin II used for treating Verotoxin		
PT	producing E. coli -		
XX			
PS	Disclosure; Fig 1b; 59pp; English.		
XX			
CC	This DNA sequence codes for the light chain variable region (see		
CC	AAV32405) of murine monoclonal antibody vtml-1 (MuVTml-1), an		
CC	antibody that specifically binds to the B subunit of verotoxin II		
CC	(VT2). The invention relates to humanised antibodies against VT2		
CC	that are capable of neutralizing VT2 and/or VT2 variants. The		
CC	humanized antibody is a humanized form of MuVTml-1 comprising the		
CC	complementarity determining regions of MuVTml-1 and heavy and		
CC	light chain variable region frameworks from the human GP4 antibody		
CC	heavy and light chain frameworks, provided that at least 1 position		
CC	selected from L49, H29, H30, H49 and H98 is occupied by the amino		
CC	acid at the equivalent position of the MuVTml-1 antibody heavy or		
CC	light chain variable region framework. Such humanized antibodies		
CC	(see AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times		
CC	that of MuVTml-1. They are used for treating a patient suffering		
CC	from, or at risk of, the toxic effects from VT2 (claimed), especially		
CC	for treating verotoxin producing Escherichia coli (VTEC) infection,		
CC	and haemolytic uraemic syndrome (HUS).		
XX			
SQ	Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;		

Best Local Similarity 83.4%; Pred. No. 1.2e-64;
Matches 267; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGCCAGCCCTCTCTCAGCCAGGAGGCGGACT 60
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DB 121 ctttcctcagggccagtcgaactattagcaaacactacactggtatcaacacaaatca 180
QY 121 GFTCAAGCCCCAAGGCTCTCATCAAGTATCGTTCACGATCCATCTCTGGGATCCCGCC 180
DB 181 catgagctcccaaggcttctcatcaagtctgtctccagtcctatctctggtatccctcc 240
QY 181 AGTTTCAGTGGCAGTGGATTCAGGACAGATTTACCCCTCACTATCTCCAGTGGAGCT 240
DB 241 aggttcagtggtgagtcagggagagattcctcctcagtcacagctggtgaaact 300
QY 241 GAAGATTTGCGAGTCTATTACTGTCACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
DB 301 gaagatttggaatgattcttgctcaacagagttacagctggtcgctcagttcgtgct 360
QY 301 GGGACCAAGTGGAAATTTAA 320
DB 361 gggaccaagctggagctgaa 380

RESULT 15

AAAA4346

ID AAA44346 standard; cDNA; 651 BP.

XX AC AAA44346;

DT 21-AUG-2000 (first entry)

DE Human secreted expressed sequence tag SEQ ID NO:921.

XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
KW antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW vaccine; autoimmunity disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.

OS Homo sapiens.

XX WO200021991-A1.

PN 20-APR-2000.

PD 15-OCT-1999; 99WO-US24206.

PF 15-OCT-1998; 98US-0104436.

PR (GENY) GENETICS INST INC.

XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

XX WPI: 2000-317938/27.

XX Isolated polynucleotides, and encoded proteins, comprising secreted

PT expressed sequence tags (SESTs), useful for treating various disorders

PT such as autoimmune, infectious, and central nervous system disorders -

XX Claim 1; Page 440; 803pp; English.
XX
CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;

Query Match 72.8%; Score 233.6; DB 21; Length 651;
Best Local Similarity 83.1%; Pred. No. 4.8e-64;
Matches 266; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGCCAGCCCTCTCTCAGCCAGGAGGCGGACT 60
DB 94 gatattgtgactcagctccagccctgtctgtgactccagagatagatgctct 153
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DB 154 ctttcctcagggccagtcgaactattagcaaacactacactggtatcaacacaaatca 213
QY 121 GGTCAAGCCCCAAGGCTCTCATCAAGTATCGTTCACGATCCATCTCTGGGATCCCGCC 180
DB 214 catgagctcccaaggcttctcatcaaatatgctcccaatccatctctggtatccctcc 273
QY 181 AGTTTCAGTGGCAGTGGATTCAGGACAGATTTACCCCTCACTATCTCCAGTGGAGCT 240
DB 274 aggttcagtggtgagtcagggagagattcctcctcagtcacagctggtgaaact 333
QY 241 GAAGATTTGCGAGTCTATTACTGTCACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
DB 334 gaagatttggaatgattcttgctcaacagagttacagctggtgaaact 393
QY 301 GGGACCAAGTGGAAATTTAA 320
DB 394 gggaccaagctggaaataaa 413

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:12 ; Search time 87.94 seconds
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691.027 Million cell updates/sec

Title: US-08-791-391a-3
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Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	77.3	381	1	US-07-634-278-82
2	248	77.3	381	1	US-08-477-728-82
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4	248	77.3	381	1	US-08-487-200-82
5	248	77.3	381	4	US-08-484-537-82
6	248	77.3	424	1	US-08-436-463-3
7	241.6	75.3	5238	6	5453363-1
8	227.2	70.8	321	2	US-08-232-081B-35
9	224	69.8	321	2	US-08-232-081B-36
10	224	69.8	324	2	US-08-737-560A-13
11	224	69.8	363	2	US-08-737-560A-8
12	216	67.3	322	2	US-08-476-176B-3
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14	216	67.3	322	3	US-08-485-246A-3
15	206.4	64.3	321	2	US-08-232-081B-39
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19	201.2	62.7	720	2	US-08-800-198-7
20	201.2	62.7	720	3	US-09-296-595-7
21	200	62.3	720	2	US-07-956-399-1
22	196.2	61.1	429	2	US-08-653-402B-7
23	193.6	60.3	321	1	US-08-192-102-2
24	193.6	60.3	321	1	US-08-324-799-2
25	193.6	60.3	321	2	US-08-192-861A-2
26	193.6	60.3	717	2	US-07-956-399-3
27	187.6	58.4	812	1	US-08-053-131-178

28	187.6	58.4	812	1	US-08-096-762-178
29	187.6	58.4	812	4	US-09-042-353-41
30	181.2	56.4	900	1	US-08-053-131-180
31	181.2	56.4	900	1	US-08-096-762-180
32	181.2	56.4	900	4	US-09-042-353-43
33	180.8	56.3	931	3	US-09-049-672A-19
34	174.8	54.5	321	4	US-09-240-274-201
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38	174.2	54.3	325	5	PCT-US93-12501-1
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41	174	54.2	642	3	US-08-837-058-10
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44	172.8	53.8	424	3	US-08-485-246A-7
45	172.2	53.6	321	4	US-09-240-274-216

ALIGNMENTS

RESULT 1
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
;
US-07-634-278-82

Query Match          77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
   |||||||
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 120
   |||||||
QY 61 CTTTCCTGCCAGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCCT 120
   |||||||
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   |||||||
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
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QY 181 AGGTTGAGTGGCAGTGGATCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
   |||||||
Db 241 AGGTTGAGTGGCAGTGGATCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 300
   |||||||
QY 241 AGGTTGAGTGGCAGTGGATCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 300
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Db 301 GAAGATTTGGAAATGATTTCTGTCAACAGAGTAACAGTTGGCCCTCATACGTTCCGAGGG 360
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QY 301 GGGACCAAGGTGGAATAA 320
   |||||||
Db 361 GGGACCAAGCTGGAATAA 380
   |||||||

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
;
US-08-477-728-82

Query Match          77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
   |||||||
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 120
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QY 61 CTTTCCTGCCAGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCCT 120
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Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 240
   |||||||
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   |||||||
Db 241 AGGTTGAGTGGCAGTGGATCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 300
   |||||||
QY 241 GAAGATTTGGAAATGATTTCTGTCAACAGAGTAACAGTTGGCCCTCATACGTTCCGAGGG 300
   |||||||
Db 301 GAAGATTTGGAAATGATTTCTGTCAACAGAGTAACAGTTGGCCCTCATACGTTCCGAGGG 360
   |||||||
QY 301 GGGACCAAGGTGGAATAA 320
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Db 361 GGGACCAAGCTGGAATAA 380
   |||||||

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
; US-08-474-040-82

```

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Query Match 77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCGAGAGAAAGGCGACT 60
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
Qy 61 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCCTACACTGTGTATCAACAAGGCGCT 120
Db 121 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCCTACACTGTGTATCAACAAGGCGCT 180
Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 120
Db 181 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 180
Qy 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 240
Db 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 300
Qy 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAGCAGCTTGGAGGG 300
Db 301 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAGCAGCTTGGAGGG 360
Qy 301 GGGACCAAGGTGGAAATTA 320
Db 361 GGGACCAAGGTGGAAATTA 380

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RESULT 4
US-08-487-200-82
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.

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; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
; US-08-487-200-82

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Query Match 77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCGAGAGAAAGGCGACT 60
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120
Qy 61 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCCTACACTGTGTATCAACAAGGCGCT 120
Db 121 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCCTACACTGTGTATCAACAAGGCGCT 180
Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 120
Db 181 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 180
Qy 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 240
Db 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 240
Qy 181 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATCGTTCACCAACCTACACTGTGTATCAACAAGGCGCT 240

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Db 241 AGGTTTCAGTGGCAGTGAGTACAGGACAGATTTCACCTCTCAGTGTCTCAACGGTGTGGAGACT 300
QY 241 GAAGATTTTGGCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 301 GAAGATTTTGGAGTATTCTCTCAACAGAGTAACAGTTGGCCTCATAGTTTCGGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 5
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend Khourie and Crew
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,375
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-484-537-82

Query Match 77.3%; Score 248; DB 4; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;

Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 GAGATTTGCTTAAGTCTCAGTCTCAGCCAGCCCTGCTCTCAGCCAGGAGAAAGGGGAGCT 60
Db 61 GATATTGCTTAAGTCTCAGTCTCAGCCAGCCCTGCTCTCAGCCAGGAGATAGCGTCAGT 120
QY 61 CTTTCTCGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTGTATCAACAAGGCGCT 120
Db 121 CTTTCTCGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTGTATCAACAAGTATCA 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180
Db 181 CATGAGTCTTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 240
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCAGTCTCAGTGTCAACGGTGTGGAGCT 240
Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCAGTCTCAGTGTCAACGGTGTGGAGCT 300
QY 241 GAAGATTTTGCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 301 GAAGATTTTGGAGTATTCTCTCAACAGAGTAACAGTTGGCCTCATAGTTTCGGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 6
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 23..403
US-08-436-463-3

Query Match 77.3%; Score 248; DB 1; Length 424;
Best Local Similarity 85.9%; Pred. No. 3e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGCTCTCAGCCCGAGGAGGAGGCGACT 60
DB 83 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTCTGACTCCAGGAGATAGCGTCAGT 142
QY 61 CTTTCTGCGCCAGCGCCAGGCTTCTCAATCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 143 CTTTCTGCGCCAGCGCCAGGCTTCTCAATCAAGTATTAGCAACACCTACACTGGTATCAACAAGTATCA 202
QY 121 GGTCAAGCCCAAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 180
DB 203 CATGAGTCTCAAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 262
QY 181 AGGTTCAAGTCCAGTCCAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 240
DB 263 AGGTTCAAGTCCAGTCCAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 322
QY 241 GAAGATTTTGCAGTCTTACTGTCAACAGAGTGGCAGCTGGCTCACACGTTCCGAGGG 300
DB 323 GAAGATTTTGCAGTCTTACTGTCAACAGAGTGGCAGCTGGCTCACACGTTCCGAGGGTCT 382
QY 301 GGGACCAAGTGGAAATTA 320
DB 383 GGGACCAAGTGGAGCTGAA 402

RESULT 7

5453363-1
PATENT NO. 5453363
APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
ING AFTER GENETIC EXPRESSION IN PROKARYOTES
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,044
FILING DATE: 02-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 942,370
FILING DATE: 09-SEP-1992
APPLICATION NUMBER: 498,500
FILING DATE: 23-MAR-1990
APPLICATION NUMBER: 76,207
FILING DATE: 23-OCT-1986
SEQ ID NO: 1:
LENGTH: 5238
5453363-1

Query Match 75.3%; Score 241.6; DB 6; Length 5238;
Best Local Similarity 84.7%; Pred. No. 8.7e-68;
Matches 271; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGCTCTCAGCCCGAGGAGGAGGCGACT 60
DB 7 gatattgttaactcagttccagccacctgtctgtgactccaagagatagcgtcagt 66
QY 61 CTTTCTGCGCCAGCGCCAGGCTTCTCAATCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 67 ctttcctgcagggccagccaaagtattagcaacaacctacactggtatcaacaataatca 126
QY 121 GGTCAAGCCCAAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 180
DB 127 catgagtcctcaaggtctctcaataatgctctccagtgcca tctctg99gagctccctct 186
QY 181 AGGTTCAAGTGGCAGTGGAGTGGAGGACAGATTTTCAACCCCTCACTATCTCCAGTCTGGAGCGCT 240

DB 187 aggttcagtgagtgatcagggacagagatttctcagttatcaaacagtgtagagact 246
QY 241 GAAGATTTTGCAGTCTTACTGTCAACAGAGTGGCAGCTGGCTTCACACGTTCCGAGGG 300
DB 247 gaagattttggaatgtatttctgtcaacagagtaacagctggcctctcacgttcggtgct 306
QY 301 GGGACCAAGTGGAAATTA 320
DB 307 gggaccaagctggagctgaa 326

RESULT 8

US-08-232-081B-35
Sequence 35: Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WILDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-35

Query Match 70.8%; Score 227.2; DB 2; Length 321;
Best Local Similarity 81.9%; Pred. No. 1.2e-63;
Matches 262; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGCTCTCAGCCCGAGGAGGAGGCGACT 60
DB 1 GAGATCGTCTGACTCAGTCTCCAGGCACACTGCTCTGAGTCCAGGAGAGAGGCCACA 60
QY 61 CTTTCTGCGCCAGCGCCAGGCTTATAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 61 CTGTCCTGCGAGGCGAGTCCAGCCATTGGCAAGACATACACTGGTATCAAGAGAGCCA 120
QY 121 GGTCAAGCCCAAGGCTTCTCAATCAAGTATTAGTGTCCAGTCCATCTCTGGGATCCCGGCC 180
DB 121 GGCCTAGGCCCAAGGCTTCTCAATCAAGTATTAGTGTCTGAGTCTATCTCTGGGATCCCTGAT 180
QY 181 AGGTTCAAGTGGCAGTGGAGTGGAGGACAGATTTTCAACCCCTCACTATCTCCAGTCTGGAGCGCT 240

Db 181 AGGTTAGTGGCAGGTGGATCAGGACAGATTTTACTCTTACAACTCCAGGCTGGAGCCA 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTAGTAGTGGCCGCTACGTTCCGTCAG 300
QY 301 GGGACCAAGGTGGAATAA 320
Db 301 GGGACCAAGGTGAGATAAA 320

RESULT 9

US-08-232-081B-36
; Sequence 36, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDNES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-232-081B-36

Query Match 69.8%; Score 224; DB 2; Length 321;
Best Local Similarity 81.2%; Pred. No. 1.2e-62;
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGAAAGGCGGACT 60
Db 1 GAGATCGCTCTGACTCAGTCCTCAGGACACTGTCTGTGAGTCCAGGAGAAAGGCCACA 60
QY 61 CTTTCCTGCCAGGCCAGCAAGATATTAGCAACCACTACACTGTATCATCAAAAGGCGCT 120
Db 61 CGTCTCTGAGGCCGAGTCAGACCACTTGCAACGATACACTGTGTATCAGCAGAGACCA 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGATCCCGCC 180
Db 121 GGGCAGGCCGCCAAGGCTTCTCATATATTATGTTCTGTGAGTCTATCTCTGGCATCCCTGAT 180
QY 181 AGGTTTCAGTGGCAGTGGATCAGGAGACAGATTTTCAACCCCTCACTATCTCCAGTCTGAGCGCT 240

Db 181 AGGTTAGTGGCAGGTGGATCAGGACAGATTTTACTCTTACAACTCCAGGCTGGAGCCA 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTAGTAGTGGCCGCTACGTTCCGTCAG 300
QY 301 GGGACCAAGGTGGAATAA 320
Db 301 GGGACCAAGGTGAGATAAA 320

RESULT 10

US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737.560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
US-08-737-560A-13

Query Match 69.8%; Score 224; DB 2; Length 324;
Best Local Similarity 81.2%; Pred. No. 1.2e-62;
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGAAAGGCGGACT 60

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; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain
; OTHER INFORMATION: variable region
; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1
; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2
; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3
; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region
;
US-08-737-560A-8
Query Match 69.8%; Score 224; DB 2; Length 363;
Best Local Similarity 81.2%; Pred. No. 1.3e-62;
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 1 GAGATTGTGATGACCCAGTCTCCAGCCAGCTGTGTGACTCCAGGAGATAGAGTCTCT 60
Db 1 GACATTGTGATGACCCAGTCTCCAGCCAGCTGTGTGACTCCAGGAGATAGAGTCTCT 60
Qy 61 CTTTCTCCAGCCAGCCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCT 120
Db 61 CTTTCTCCAGCCAGCCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGTCA 120
Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
Db 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
Qy 181 AGGTTTTCAGTCTATTACTGTCAACAGAGTGCAGCTGCCTCCACACCTTCGGAGGG 300
Db 181 AGGTTTTCAGTCTATTACTGTCAACAGAGTGCAGCTGCCTCCACACCTTCGGAGGG 300
Qy 301 GGGACCAAGCTGGAATCAA 320
Db 301 GGCACCAAGCTGGAATCAA 320

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RESULT 11

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US-08-737-560A-8
; Sequence 8, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuil
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA: US/08737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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RESULT 12

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US-08-476-176B-3
; Sequence 3, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:

```


STATE: New Jersey
 COUNTRY: USA
 ZIP: 07936-1080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,246A
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/127,721
 FILING DATE: 27-SEPTEMBER-1993
 APPLICATION NUMBER: US 07/952,802
 FILING DATE: 25-SEPTEMBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6072035ak, Henry P.
 REGISTRATION NUMBER: 33,200
 REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 277-5110
 TELEFAX: (908) 277-4306
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 322 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..321
 OTHER INFORMATION: /product= "light chain variable
 OTHER INFORMATION: domain of murine antibody TES-C21"
 US-08-485-246A-3

Query Match 67.3%; Score 216; DB 3; Length 322;
 Best Local Similarity 79.7%; Pred. No. 4.5e-60;
 Matches 255; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
 Db 1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAAGTCACT 60

Qy 61 CTTTCCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCT 120
 Db 61 TTCTCTCGAGGCGCAGTCAAGTATTGGCACAACATACACTGGTATCAACAAGAAACA 120

Qy 121 GGTCAGCCCCAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180
 Db 121 GATGTTCTCCAAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180

Qy 181 AGGTTAGTGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240
 Db 181 AGGTTAGTGCAGTGGATCAGGACAGATTTACTCTAAACATCAACAGTGTGGAGTCT 240

Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTTCACACGTTCCGAGGG 300
 Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTATAGTCTGGCCAAACACCTTCGAGGG 300

Qy 301 GGGACCAAGTGGAAATTA 320
 Db 301 GGGACCAAGTGGAGATAAA 320

RESULT 15
 US-08-232-081B-39
 ; Sequence 39, Application US/08232081B
 ; Patent No. 5886152
 ; GENERAL INFORMATION:

APPLICANT: NAKATANI, TOMOYUKI
 APPLICANT: GOMI, HIDEYUKI
 APPLICANT: WIJDENES, JOHN
 APPLICANT: NOGUCHI, HIROSHI
 TITLE OF INVENTION: HUMANIZED B-B10
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,081B
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: SVENSSON, LEONARD R
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 20-3484
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..321
 US-08-232-081B-39

Query Match 64.3%; Score 206.4; DB 2; Length 321;
 Best Local Similarity 77.8%; Pred. No. 5.2e-57;
 Matches 249; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
 Db 1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAAGTCACT 60

Qy 61 CTTTCCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCT 120
 Db 61 TTCTCTCGAGGCGCAGTCAAGTATTGGCACAACATACACTGGTATCAAGGAAGAACA 120

Qy 121 GGTCAGCCCCAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180
 Db 121 AATGTTCTCCAAAGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCCGCC 180

Qy 181 AGGTTAGTGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240
 Db 181 AGGTTAGTGCAGTGGATCAGGACAGATTTACTCTTAGCATCAACAGTGTGGAGTCT 240

Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTTCACACGTTCCGAGGG 300
 Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTATAGTCTGGCCGCTCAGCTTCGGTGT 300

Qy 301 GGGACCAAGTGGAAATTA 320
 Db 301 GGGACCAAGTGGAGCTGAA 320

Search completed: October 11, 2001, 15:14:14

Job time: 5001 sec

A;Residues: 1-111 <OLE>

A:Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 459; DB 2; Length 111;
Best Local Similarity 83.2%; Pred. No. 1.1e-33;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYKRSQISGIPA 60
|||||
Db 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYDASNRATGIPA 60
|||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||

RESULT 3
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are new
A:Reference number: A56701; MUID:95279371
A:Accession: A56701
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:g762824
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 457; DB 2; Length 128;
Best Local Similarity 82.2%; Pred. No. 2e-33;
Matches 88; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYKRSQISGIPA 60
|||||
Db 21 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYDASNRATGIPA 80
|||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 81 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 127
|||||

RESULT 4
S40379
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40379
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40379
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72489; NID:g441446; PIDN:CAA51157.1; PID:g441447
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match* 81.3%; Score 456; DB 2; Length 128;

Best Local Similarity 81.3%; Pred. No. 2.4e-33;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYKRSQISGIPA 60
|||||
Db 21 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYASNRATGIPA 80
|||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 81 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 127
|||||

RESULT 5
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: B45722; MUID:93100833
A:Accession: B45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 453; DB 2; Length 107;
Best Local Similarity 76.6%; Pred. No. 3.7e-33;
Matches 82; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYKRSQISGIPA 60
|||||
Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSIHNLHWYQORSHSPRLLIKYASQISGIPS 60
|||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||

RESULT 6
S54905
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S54905
R:Esposito, G.; Traboni, C.
submitted to the EMBL Data Library, November 1994
A:Description: Cloning and sequencing of cDNA coding for the variable domains of a hu
A:Reference number: S54905
A:Accession: S54905
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <ESP>
A:Cross-references: EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PID:g809555
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 451.5; DB 2; Length 114;
Best Local Similarity 80.6%; Pred. No. 5.3e-33;
Matches 87; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYKRSQISGIPA 60
|||||
Db 1 DVVMTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIYDASRRATGIPA 60
|||||

QY 61 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 107
|||||
Db 61 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 108
|||||

RESULT 7
G44151
Ig kappa chain V region (JM-10) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: G44151
R:Zebende, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: G44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-108 <2EB>
A:Cross-references: GB:M88317; NID:g183968; PIDN:AAA35975.1; PID:g183969
A:Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 450; DB 2: Length 108;
Best Local Similarity 82.7%; Pred. No. 6.8e-33;
Matches 86; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 4 LTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARFS 63
|||||

Db 3 LTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARFS 62
|||||

QY 64 GSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 107
|||||

Db 63 GSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 106
|||||

RESULT 8
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 448; DB 2: Length 123;
Best Local Similarity 75.7%; Pred. No. 1.2e-32;
Matches 81; Conservative 18; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPA 60
|||||

Db 13 DIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPS 72
|||||

QY 61 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 107
|||||

Db 73 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKLEIK 119
|||||

RESULT 9
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (A
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 447; DB 2: Length 107;
Best Local Similarity 74.8%; Pred. No. 1.2e-32;
Matches 80; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPA 60
|||||

Db 1 DIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPS 60
|||||

QY 61 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 107
|||||

Db 61 RFGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKLEIK 107
|||||

RESULT 10
PC4282
Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: PC4282; PC4284
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltra
A:Reference number: PC4279; MUID:97236289
A:Accession: PC4282
A:Molecule type: protein
A:Residues: 1-106 <SUZ>
A:Note: E-42
A:Accession: PC4284
A:Molecule type: protein
A:Residues: 1-106 <SUZ>
A:Note: E-56
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sj
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 446; DB 2: Length 106;
Best Local Similarity 81.0%; Pred. No. 1.5e-32;
Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARF 62
|||||

Db 1 VLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPAKF 60
|||||

QY 63 SGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 107
|||||

Db 61 SGSGSGTDFLTITISSELEDFAVYCCQSGSWPH-TFGGKTKVEIK 105
|||||

RESULT 11

C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40344
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:9408091
A;Accession: S40344
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <LEU>
A;Cross-references: EMBL:X72454; NID:g441376; PIDN:CRA51122.1; PID:g441377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 442; DB 2; Length 125;
Best Local Similarity 81.9%; Pred. No. 3.9e-32;
Matches 86; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 EVLTQSPATLSLSPGERATLSCAASQISINHLHWYQORFGQAPRLLIKVRQSISGIPA 60
Db 21 EVLTQSPATLSLSPGERATLSCRASQSVSTIYAWYQOIFGQAPRLLIYDASNRATGIPA 80
QY 61 RFSGSGSGTDFTLTISLEPEDFAVYYCQSGSWPHTFGGKTVE 105
Db 81 RFSGSGSGTDFTLTISLEPEDFAVYYCQORSYWPLTFGGGKTVE 125

RESULT 14
A30608
Ig kappa chain V-III region (Son) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM auto
A;Reference number: A30601; MUID:89215279
A;Accession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 439.5; DB 2; Length 109;
Best Local Similarity 81.5%; Pred. No. 5.7e-32;
Matches 88; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 EVLTQSPATLSLSPGERATLSCAASQSI-SNHLHWYQORFGQAPRLLIKVRQSISGIP 59
Db 1 EVLTQSPATLSLSPGERATLSCRASQSVSSYLAWTQKQAPRLLIYGCASRATGIP 60
QY 60 ARFSGSGSGTDFTLTISLEPEDFAVYYCQSGSWPHTFGGKTVEIK 107
Db 61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSGSPYTFGGGKTVEIK 108

RESULT 15
S29627
Ig kappa chain V region (60.3 hybridoma) - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34110; S29627
R;Wells, M.A.; Hsiao, K.; Harris, L.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
A;Reference number: S34110; MUID:93324379
A;Accession: S34110

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <WA2>
A;Cross-references: EMBL:Z17330; NID:g38511; PIDN:CAA78978.1; PID:g38512
A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 439; DB 2; Length 129;
Best Local Similarity 79.8%; Pred. No. 7.5e-32;
Matches 87; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPCQAPRLLIKYSQISGIPA 60
Db |||||||||||||||||||:||||: || |||||:||||| || | :||||
21 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPCQAPRLTIYDASNRATGIPA 80

QY 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQSGSWP--HTFGGGTKVEIK 107
Db |||||||||||||||||||: || |||||:|||||
81 RFGSGSGTDFTLTISLSEPEDFAVYYCQHRDNPWGATFGGGTKVEIK 129

Search completed: October 11, 2001, 12:02:36
Job time: 301 sec

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 group";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01892; K3HUSI.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
 Query Match 76.2%; Score 427.5; DB 1; Length 109;
 Best Local Similarity 79.6%; Pred. No. 5.2e-37;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 Db 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 107
 Db 61 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 108
 RESULT 3
 KV3L_HUMAN STANDARD; PRT; 129 AA.
 ID KV3L_HUMAN
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR; P10022; K3HUA.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109
 BY SIMILARITY.

FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
 Query Match 76.0%; Score 426.5; DB 1; Length 129;
 Best Local Similarity 79.6%; Pred. No. 8e-37;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 Db 21 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 107
 Db 81 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 128
 RESULT 4
 KV3E_HUMAN STANDARD; PRT; 109 AA.
 ID KV3E_HUMAN
 AC P01623;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 group";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR; A01896; K3HUSL.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;
 Query Match 75.1%; Score 421.5; DB 1; Length 109;
 Best Local Similarity 79.6%; Pred. No. 2.1e-36;
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 Db 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQSISGIP 59
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 107
 Db 61 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHTFGGKVEIK 108
 RESULT 5
 KV3M_HUMAN STANDARD; PRT; 129 AA.
 ID KV3M_HUMAN
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P00021; K3HUVI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 55 FRAMEWORK 2.
FT DOMAIN 56 70 FRAMEWORK 3.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 75.1%; Score 421.5; DB 1; Length 129;
Best Local Similarity 79.6%; Pred. No. 2.6e-36;
Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGQAPRLIKYRSQSISGIP 59
Db 21 EIVLTQSPATLSLSPGERATLSCQASQSVSSYLAQYQKPGQAPRLIYGAASSRATGIP 80
Qy 60 ARFGSGSGTDFTLTISLPEDFAVYCCQSGSPHPFGGKVEIK 107
Db 81 DRFGSGSGTDFTLTISRLPAXDFAVYCCQYQGGSPFWTFGGKVEIK 128

RESULT 6
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CIL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC -----
DR PIR; A01568; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
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DR EMBL; M12740; AAA58992.1; -.
DR PIR; A01898; K3HUCI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 54 FRAMEWORK 2.
FT DOMAIN 55 69 FRAMEWORK 3.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 74.4%; Score 417.5; DB 1; Length 129;
Best Local Similarity 75.9%; Pred. No. 6.6e-36;
Matches 82; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGQAPRLIKYRSQSISGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGASTRATGIPA 80
Qy 61 RFSGSGSGTDFTLTISLPEDFAVYCCQSGSW-PHFGGKVEIK 107
Db 81 RFSGSGSGTEFTLTISRLQSEDFAVYCCQYNNWPPWTFGGTRVEIK 128

RESULT 7
KV3I_HUMAN
ID KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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CC -----
DR EMBL; X01568; -.
DR PIR; A01900; K3HUVG.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
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FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 73.4%; Score 412; DB 1; Length 115;
Best Local Similarity 83.2%; Pred. No. 2.1e-35;
Matches 79; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 80
QY 61 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWP 95
DB 81 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWP 115

RESULT 8
KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN V-III REGION POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=76276460; PubMed=60899;
QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 80
QY 61 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWP 95
DB 81 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWP 115

Query Match 73.0%; Score 409.5; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 3.6e-35;
Matches 81; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIP 59
DB 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIP 60
QY 60 ARFSGSGGTFTLTISLLEPEFAVYVCOQSGSWPHTFGGKVEIK 107
DB 61 ARFSGSGGTFTLTISLLEPEFAVYVCOQSGSWPHTFGGKVEIK 108

RESULT 9
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT DOMAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.9%; Score 409; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 4.8e-35;
Matches 80; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 80
QY 61 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWPHTFGGKVEIK 107
DB 81 RFSGSGGTFTLTISLLEPEFAVYVCOQSGSWPHTFGGKVEIK 127

RESULT 10
KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6."
RL FEBS Lett. 2:301-304(1969).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01891; K3HUB6.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.

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KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 72.3%; Score 405.5; DB 1; Length 108;
Best Local Similarity 73.1%; Pred. No. 9.1e-35;
Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQIS-NHLHWYQORQGPAPRLIKYRSQISGIP 59
DB 1 ZIVLTZSPGTLSPGZRAALSCRAQLSGNYLAWYQKFGQAPRLMLYGVSSRATGIP 60

QY 60 ARFSGSGSGTDTLTISLLEPEDFAVYCCQSGSPHPTFGGKVEIK 107

DB 61 DRFSGSGSGADFTLTISRLEPEDFAVYCCQYSGSPFTFGGSKLEIK 108

RESULT 11

KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;

RT "Amino acid sequence of a light chain variable region of a human
rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies".
RL Mol. Immunol. 23:239-244(1986).

DR PIR: A01893; K3HUGO.

DR HSSP; P01789; 2WCP.

DR InterPro: IPR003006; -.

DR Pfam; PF00047; Ig 1.

KW Immunoglobulin V region.

FT DISULFID 23 89

FT NON_TER 109 109 BY SIMILARITY.

SQ SEQUENCE 109 AA; 11630 MW; 9349A5BID93588B6 CRC64;

Query Match 71.6%; Score 401.5; DB 1; Length 109;
Best Local Similarity 75.9%; Pred. No. 2.3e-34;
Matches 82; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQAS-OSISNHLHWYQORQGPAPRLIKYRSQISGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRAALSSRGYLAQYQKFGQAPRLMLYGVSSRATGIP 60

QY 60 ARFSGSGSGTDTLTISLLEPEDFAVYCCQSGSPHPTFGGKVEIK 107

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYCCQYSGSPRSGGKVEIK 108

RESULT 12

KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=77038198; PubMed=824717;

RA Capra J.D., Klapper D.G.;

RT "Complete amino acid sequence of the variable domains of two human

RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic

RT specificities".

RL Scand. J. Immunol. 5:677-684(1976).

CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.

DR PIR: A01871; KLHULY.

DR HSSP; P01607; IREI.

DR InterPro: IPR003006; -.

DR Pfam; PF00047; Ig 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 88

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match

Best Local Similarity 67.6%; Score 379; DB 1; Length 108;

Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORQGPAPRLIKYRSQISGIP 60

DB 1 DIQMTQSPSSLSVSGVDRTVITCQASQNVNAYLNWYQKPGKPLIKLYGASTREAGVPS 60

QY 61 RFSGSGSGTDTLTISLLEPEDFAVYCCQSGSPHPTFGGKVEIK 107

DB 61 RFSGSGSGTDTLTISLLEPEDFAVYCCQYNNWPTFGGKVEIK 107

RESULT 13

KV1H_HUMAN STANDARD; PRT; 108 AA.
ID KV1H_HUMAN STANDARD; PRT; 108 AA.

AC P01600;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION HAU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=71032830; PubMed=4097974;

RA Watanabe S., Hilschmann N.;

RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups".

RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01868; KLHULH.

DR HSSP; P80362; 1WTL.

DR InterPro: IPR003006; -.

DR Pfam; PF00047; Ig 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23

FT DOMAIN 24 34

COMPLEMENTARITY-DETERMINING 1.

```

QY      56  SGIPARFSGSGSDFTLTITSSLEPEDFAVYYCQSGSWPHTFGGTKVEIK 107
        ||||||| ||||| : : ||||| : ||||| |||
Db      60  SGIPARFSGSGSDFTLTINPVEADDVATYYCQSGNEDPVTFGGTKLEIK 111
        ||||||| ||||| : : ||||| : ||||| |||

RESULT 15
KV5I_MOUSE
ID      KV5I_MOUSE          STANDARD;          PRT;          115 AA.
AC      P01642;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=61220975; PubMed=6264318;
RT      Pech M., Hochtl J., Schnell H., Zachau H.G.;
RA      "Differences between germ-line and rearranged immunoglobulin V kappa
RL      coding sequences suggest a localized mutation mechanism.";
RL      Nature 291:668-670(1981).
CC      -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICING JUNCTIONS
CC      THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC      LACKING RESIDUES 17-19.
DR      PIR; A01925; KVM5L7.
DR      InterPro; IPR003006; -.
DR      Pfam; PF00047; Ig; 1.
DR      Immunoglobulin V region; Signal.
KW      SIGNAL
FT      CHAIN          1 20
FT      CHAIN          21 >115
FT      DOMAIN         21 43
FT      DOMAIN         44 54
FT      DOMAIN         55 69
FT      DOMAIN         70 76
FT      DOMAIN         77 108
FT      DOMAIN         109 >115
FT      DISULFID        43 108
FT      NON_TER        115 115
SQ      SEQUENCE      115 AA; 13615 MW; C17BEC758C577E00 CRC64;

Query Match          66.1%; Score 371; DB 1; Length 115;
Best Local Similarity 72.6%; Pred. No. 3.2e-31;
Matches 69; Conservative 12; Mismatches 14; Indels 0; Gaps
QY      1  EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLIKYRSQSISGIPA 60
        : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      21  DILTQSPATLSVPGERVSFSCRASQISGTSIHVYQORNGSPRLIKYASESISGIPS 80
        : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

QY      61  RFSGSGSDFTLTITSSLEPEDFAVYYCQSGSWP 95
        ||||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      81  RFSGSGSDFTLTINSVESEDIADYYCQSGNSWP 115

Search completed: October 11, 2001, 12:08:43
Job time: 403 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:07:34 ; Search time 46.3 Seconds
(without alignments)
305.759 Million cell updates/sec

Title: US-08-791-391a-4

Perfect score: 561

Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQSGSWPHTFGGTRKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTRMBL16:*
- 2: sp-archaea:*
- 3: sp-bacteria:*
- 4: sp-fungi:*
- 5: sp-human:*
- 6: sp-invertebrate:*
- 7: sp-mammal:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428.5	76.4	109	4 Q9UL85	Q9UL85 homo sapien
2	427	76.1	108	4 Q9UL83	Q9UL83 mus sapien
3	426.5	76.0	109	4 Q9UL78	Q9UL78 homo sapien
4	401.5	71.6	109	4 Q9UL86	Q9UL86 mus sapien
5	384	68.4	108	4 Q9UL77	Q9UL77 mus sapien
6	371	66.1	108	4 Q9UL79	Q9UL79 mus sapien
7	365	65.1	108	4 Q9UL70	Q9UL70 mus sapien
8	361.5	64.4	107	4 Q9UL81	Q9UL81 mus sapien
9	337.5	60.2	106	5 Q9UL10	Q9UL10 schistosoma
10	333	59.4	99	11 Q9JL74	Q9JL74 mus musculus
11	333	59.2	107	11 Q9JL84	Q9JL84 mus musculus
12	332	59.2	298	11 Q9QYF0	Q9QYF0 mus musculus
13	330	58.8	214	11 Q9RIA5	Q9RIA5 mus musculus
14	325	57.9	101	11 Q9JL78	Q9JL78 mus musculus
15	314	56.0	107	11 Q9ERZ9	Q9ERZ9 mus musculus
16	313	55.8	103	11 Q9JL80	Q9JL80 mus musculus
17	308	54.9	97	11 Q9JL76	Q9JL76 mus musculus
18	308	54.9	114	4 Q9UL80	Q9UL80 mus sapien
19	306.5	54.6	104	11 Q9JL82	Q9JL82 mus musculus

ALIGNMENTS

RESULT	1	280	49.9	109	6	Q9NOW5	Q9n0w5 oryctolagus
Q9UL85	21	235	41.9	107	4	Q9UL82	Q9ul82 homo sapien
ID	22	216.5	38.6	107	4	Q9NSD6	Q9nsd6 homo sapien
Q9UL85	23	182.5	32.5	109	11	Q9ETI3	Q9eti3 mus musculus
AC	24	167	29.8	130	4	Q9NP29	Q9np29 homo sapien
Q9UL85	25	154.5	27.5	135	4	Q9H524	Q9h524 homo sapien
AC	26	150	26.7	93	4	Q9UL76	Q9ul76 homo sapien
Q9UL85	27	145	25.8	123	11	Q61243	Q61243 mus musculus
AC	28	134	23.9	168	4	Q9UQ56	Q9uq56 homo sapien
Q9UL85	29	126	22.5	342	13	Q9IB00	Q9ib00 spherooides
AC	30	124.5	22.2	334	13	Q9IB05	Q9ib05 spherooides
Q9UL85	31	123.5	22.0	331	13	Q9IB07	Q9ib07 spherooides
AC	32	121.5	21.7	509	11	Q08907	Q08907 mus musculus
Q9UL85	33	121.5	21.7	509	11	Q9WTN4	Q9wtN4 mus musculus
AC	34	120	21.4	100	6	Q77624	Q77624 bos taurus
Q9UL85	35	118	21.0	152	13	Q9YH11	Q9yhl1 ginglymosto
AC	36	117	20.9	122	4	Q9UL84	Q9ul84 homo sapien
Q9UL85	37	116	20.7	340	13	Q9IAZ6	Q9iaz6 spherooides
AC	38	115.5	20.6	109	11	Q9JL75	Q9jl75 mus musculus
Q9UL85	39	115.5	20.6	509	11	Q9QX57	Q9qx57 mus musculus
AC	40	115.5	20.6	513	11	P97797	P97797 mus musculus
Q9UL85	41	115	20.5	100	13	Q9YH19	Q9yhl9 ginglymosto
AC	42	114.5	20.4	119	4	Q9UL94	Q9ul94 homo sapien
Q9UL85	43	114.5	20.4	340	13	Q9IAZ0	Q9iaz0 spherooides
AC	44	113.5	20.2	113	4	Q9UL90	Q9ul90 homo sapien
Q9UL85	45	113	20.1	136	13	Q9YHR9	Q9yhr-9 ginglymosto

ALIGNMENTS

RESULT 1

Q9UL85 PRELIMINARY; PRT; 109 AA.

AC Q9UL85; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-98277139; PubMed-9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

CC EMBL; AF035029; AAD56265.1; -

DR HSSP; P01607; IREI.

DR InterPro; IPR003006; -

DR	InterPro; IPR003596; -						
DR	Pfam; PF00047; Ig; 1.						
DR	SMART; SM00406; IGV; 1.						
FT	NON_TER 1						
FT	NON_TER 109						
SQ	SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;						
Query Match	76.4%;	Score 428.5;	DB 4;	Length 109;			
Best Local Similarity	78.7%;	Pred. No. 2.le-40;					
Matches	85;	Conservative 10;	Mismatches 12;	Indels 1;	Gaps 1;		
Qy	1	EIVLTQSPATLSLSPGERATLSQASQSTSNHLHWYQQPGQAPRLILIKYRQSTSGIPA	60				
Db	1	EIVLTQSPATLSVSPGERATLSQASQSTSNHLHWYQQPGQAPRLILIKYRQSTSGIPA	60				
Qy	61	RFGSGSGTDFLTITSSLEPEDFAVYQQSGSWPH-TFGGTRKVEIK	107				

DR EMBL; AF035036; AAD56272.1; -.

AC · Q9UL77;

```
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 68.4%; Score 384; DB 4; Length 108;
Best Local Similarity 69.2%; Pred. No. 1.9e-35;
Matches 74; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPGQAPRLLIKYSQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITCRASQGISNLYNQKPKGAPKAPLLIYAASLQSGVPS 60
Qy 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQSGSWPHTFGGKTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQSYSTSWTEGKTKVEIK 107

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79;
AC Q9UL79;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;
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Query Match 66.1%; Score 371; DB 4; Length 108;
Best Local Similarity 67.3%; Pred. No. 5.4e-34;
Matches 72; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPGQAPRLLIKYSQSISGIPA 60
Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISNLYNQKPKGAPKAPLLIYAASLQSGVPS 60
Qy 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQSGSWPHTFGGKTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQYYSFPPTFGGKTKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 65.1%; Score 365; DB 4; Length 108;
Best Local Similarity 64.5%; Pred. No. 2.5e-33;
Matches 69; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPGQAPRLLIKYSQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITCRASQGISNLYNQKPKGAPKAPLLIYAASLQSGVPS 60
Qy 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQSGSWPHTFGGKTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLEPEDFVAVYCCQKYNAPRTFGGKTKLEIK 107

RESULT 8
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```


QY 10 TSLSPGERATLSQASQSI-SNHLHWYQORPQOAPRLLIKYRSQTSIGIPARFSGSG 68
Db 2 TMAASPEKITITCSASSISSNYLHWYQKPGFSPKLLIYRTSNLASGVPTFRFSGSG 61
QY 69 TDTLTITISLEPEFAVYCYQSGSWP-WTFGGGKVEIK 107
Db 62 TSYSLTIGTMEADVATYCYQSGSSIPRYTFGGGKLEIK 101

RESULT 15

O9ERZ9
ID Q9ERZ9 PRELIMINARY; PRT; 107 AA.
AC Q9ERZ9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 56.0%; Score 314; DB 11; Length 107;
Best Local Similarity 54.2%; Pred. NO. 1.2e-27;
Matches 58; Conservative 22; Mismatches 21; Indels 6; Gaps 1;

QY 4 LTQSPATLSLSPGERATLSQASQSI-----SNHLHWYQORPQOAPRLLIKYRSQTSIG 57
Db 1 MTQSPSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAQYQKPGQSPPELLVYFASTRESG 60
QY 58 IPARFSGSGSGTDTLTITISLEPEFAVYCYQSGSWPHTFGGKTV 104
Db 61 VPDREMGSGSGTDTLTITISSVQTDLADYFCQGHYRTPTFGSGTKL 107

Search completed: October 11, 2001, 12:07:34
Job time: 409 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:57 ; Search time 44.8 Seconds
(without alignments)
144.794 Million cell updates/sec

Title: US-08-791-391a-4

Perfect score: 561

Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQSGSPHPTFGSGTKRVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	19 AAW76002	Vitaxin antibody 1
2	561	100.0	107	22 AAB61360	Vitaxin light chain
3	555	98.9	107	19 AAW76006	LM609 grafted anti
4	555	98.9	107	22 AAB61364	Light chain variab
5	512	91.3	107	13 AAR25729	Humanised VL regio
6	512	91.3	107	22 AAB69678	Humanised CMV5 ant
7	512	91.3	107	22 AAB69690	Human Wol antibody
8	510	90.9	107	20 AAW84098	Humanised anti-alp
9	510	90.9	112	20 AAW84100	Vitronectin alpha-
10	507	90.4	127	18 AAW08946	Kappa light chain
11	501	89.3	107	18 AAW08948	Kappa light chain

12	494	88.1	107	18 AAW08949	Kappa light chain
13	490	87.3	127	21 AAY32407	Mouse anti-verotox
14	489	87.2	107	20 AAY30205	The variable light
15	488	87.0	107	20 AAY30203	The variable light
16	486	86.6	127	15 AAR50192	Light chain variab
17	486	86.6	127	20 AAY26982	Light chain variab
18	484	86.3	107	14 AAR37612	hIL2R Ab L chain v
19	483	86.1	107	21 AAY71240	Humanised antibody
20	480	85.6	107	21 AAY70604	Vkappa region of h
21	480	85.6	127	15 AAR50187	Light chain variab
22	480	85.6	127	20 AAY26980	Light chain variab
23	480	85.6	245	21 AAY70605	scfv fragment of h
24	477	85.0	127	15 AAR50191	Light chain variab
25	477	85.0	127	20 AAY26981	Light chain variab
26	470	83.8	107	19 AAY76004	LM609 antibody lig
27	470	83.8	107	22 AAB61362	Antibody LM609 lig
28	459	81.8	107	21 AAY71238	Humanised antibody
29	456	81.3	105	20 AAW87456	Humanised antibody
30	456	81.3	105	20 AAW87458	Humanised anti-alp
31	455	81.1	109	20 AAY06380	Murine monoclonal
32	454	80.9	107	22 AAB66414	Human Fab clone LD
33	449.5	80.1	108	22 AAB72884	Human anti-HER2/ne
34	448.5	79.9	107	18 AAW24513	Anti-Factor-IX hum
35	447	79.7	107	22 AAB69677	Murine CMV5 antibo
36	447	79.7	127	22 AAB69687	Murine CMV5 antibo
37	445	79.3	214	20 AAY08599	Anti-human TNF-alp
38	444	79.1	127	15 AAR54093	Sequence of mouse
39	440	78.4	109	15 AAR52033	Light chain variab
40	439	78.3	349	12 AAR12128	181 IgG aberrant 1
41	439	78.3	401	12 AAR12129	ORF 1 of IgG light
42	439	78.3	414	12 AAR13111	181 IgG aberrant 1
43	439	78.3	414	12 AAR13018	181 IgG aberrant 1
44	437.5	78.0	109	22 AAB62756	Human HIV-1 monocl
45	437	77.9	107	14 AAR386601	HYH light chain.

ALIGNMENTS

RESULT 1

AAW76002
ID AAW76002 standard; Protein; 107 AA.

XX
AC AAW76002;

XX
DT 02-NOV-1998 (first entry)

XX
DE Vitaxin antibody light chain variable region protein fragment.

XX
KW Vitaxin; antibody; variable region; heavy chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis.

XX
OS Mus sp.

XX
PN WO9833919-A2.

XX
PD 06-AUG-1998.

XX
PF 30-JAN-1998; 98WO-US01826.

XX
PR 30-JAN-1997; 97US-0791391.

XX
PA (IXSY-) IXSYS INC.

XX
PI Glaser SM, Huse WD;

XX
DR WPI; 1998-437472/37.

XX
DR N-PSDB; AAW49621.

XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX Claim 1; Fig 1b; 129pp; English.
 XX This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX Sequence 107 AA;

Query Match 100.0%; Score 561; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQQRPGQAPRLLIKYSQISGIPA 60
 |||||
 Db 1 elvltqspatlsispgeratlsqasqsisnhlhwqqrpgqaprllikyrsgisgipa 60
 |||||

QY 61 RFGSGSGTDFTLTISLSPEDFAVYQCQSGSWPHTFGGKVEIK 107
 |||||
 Db 61 rfsgsgsgtdftltisslepedfavyccqsgswphtfgggtkveik 107
 |||||

RESULT 2

AAAB61360
 ID AAB61360 standard; protein; 107 AA.
 XX
 AC AAB61360;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Vitaxin light chain variable region protein.
 XX
 KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 XX
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 PS Disclosure; Fig 1; 132pp; English.
 XX
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta_3 integrin or
 CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of
 CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX Sequence 107 AA;

Query Match 100.0%; Score 561; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQQRPGQAPRLLIKYSQISGIPA 60
 |||||
 Db 1 elvltqspatlsispgeratlsqasqsisnhlhwqqrpgqaprllikyrsgisgipa 60
 |||||

QY 61 RFGSGSGTDFTLTISLSPEDFAVYQCQSGSWPHTFGGKVEIK 107
 |||||
 Db 61 rfsgsgsgtdftltisslepedfavyccqsgswphtfgggtkveik 107
 |||||

RESULT 3

AAW76006
 ID AAW76006 standard; Protein; 107 AA.
 XX
 AC AAW76006;
 XX
 DT 02-NOV-1998 (first entry)
 XX
 DE LM609 grafted antibody light chain variable region protein fragment.
 XX
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 49
 FT /label= Arg, Met
 XX
 PN WO9833919-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US01826.
 XX
 PR 30-JAN-1997; 97US-0791391.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Glaser SM, Huse WD;
 XX
 DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49843.
 XX
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 PS Claim 19; Fig 7; 129pp; English.
 XX
 CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in

CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 107 AA;

Query Match 98.9%; Score 555; DB 19; Length 107;
Best Local Similarity 99.1%; Pred. No. 1e-35;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQQSGWPHTFGGKVEIK 60
Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQQSGWPHTFGGKVEIK 60
QY 61 RFGSGSGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107
Db 61 RFGSGSGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

RESULT 4

AAB61364
ID AAB61364 standard; protein; 107 AA.

AC AAB61364;

DT 03-APR-2001 (first entry)

DE Light chain variable region of LM609.

KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.

OS Unidentified.

PN W0200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPT; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -

PS Disclosure; Fig 7; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX Sequence 107 AA;

Query Match 98.9%; Score 555; DB 22; Length 107;
Best Local Similarity 99.1%; Pred. No. 1e-35;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQQSGWPHTFGGKVEIK 60
Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQQSGWPHTFGGKVEIK 60

QY 61 RFGSGSGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107
Db 61 RFGSGSGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

RESULT 5

AAR25729
ID AAR25729 standard; Protein; 107 AA.

AC AAR25729;

DT 13-JAN-1993 (first entry)

XX Humanised VL region of the mouse CMV5 antibody.

KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
KW gH; light chain; variable region; framework; human; Wol.

OS Mus musculus.

FH Key Location/Qualifiers
FT Region 24..34 /note= "CDR"

FT Region 50..56 /note= "CDR"

FT Region 89..97 /note= "CDR"

FT Misc-difference 49 /note= "mutated residue"

XX W09211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(s) having murine CDRs in human framework
PT regions - have lower antigenicity; useful for treating e.g. HSV,
PT CMV, T-cell disorders, myeloid disorders and auto-immune
PT conditions

XX Claim 40; Fig 27A; 141pp; English.

XX The sequence shows the humanised mature light chain variable
CC region of the mouse CMV5 antibody. Murine CDRs were used
CC in a human Wol framework to produce a pure humanised immunoglobulin
CC (Ig) which is capable of binding to the gH glycoprotein of
CC cytomegalovirus. The Ig is non immunogenic, due to the human
CC framework, and has a strong affinity for its predetermined
CC antigen. They can be produced in large quantities via recombinant
CC DNA and monoclonal antibody technology. The humanised Igs may be
CC used alone or in combination with chemotherapeutic agents such as
CC non-steroidal anti-inflammatory drugs or immunosuppressants.
CC See also AAR25721-32.

```
SQ Sequence 107 AA;
Query Match 91.3%; Score 512; DB 13; Length 107;
Best Local Similarity 91.6%; Pred. No. 2e-32; 6; Indels 0; Gaps 0;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 eivltqspgtlsispgeratlsqcrasqisnlnhwqqkpgqprllikyasqsigp 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 61 RFGSGSGDTFTLTISLEPEDFAVYYCQSGSWPHFTFGGKTVEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 rfsgsgsgdtftltisrlepedfavyycqsgsnwphftfggktveik 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 7
AAB69678
ID AAB69678 standard; Protein; 107 AA.
XX
AC AAB69678;
XX
DT 30-APR-2001 (first entry)
XX
DE Human WOI antibody light chain SEQ ID NO: 87.
XX
KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
light chain; graft versus host disease; transplant; autoimmune disease;
multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
OS Homo sapiens.
XX
PN US6180370-B1.
XX
PD 30-JAN-2001.
XX
PF 07-JUN-1995; 95US-0484537.
XX
PR 28-DEC-1988; 88US-0290975.
PR 13-FEB-1989; 89US-0310252.
PR 28-SEP-1990; 90US-0590274.
PR 19-DEC-1990; 90US-0634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX
XX Producing humanized immunoglobulin, involves producing a cell
containing DNA segments encoding humanized heavy and light chain
variable regions, and expressing the DNA segments in the cell -
Example 8; Fig 6; 145pp; English.
XX
XX The present invention describes a method of producing humanised
immunoglobulins involving expressing in a cell a nucleic acid encoding a
humanised version of an immunoglobulin. This is obtained by comparing a
donor and human immunoglobulin and producing a combined antibody which
contains part of each. These are useful in the treatment of
graft-versus-host disease, transplant rejection, autoimmune diseases such
as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
and systemic lupus erythematosus, herpes infections, CMV virus infections
and myeloid leukaemia. The present sequence is an antibody used to
demonstrate the method of the invention.
XX
SQ Sequence 107 AA;
Query Match 91.3%; Score 512; DB 22; Length 107;
Best Local Similarity 91.6%; Pred. No. 2e-32; 6; Indels 0; Gaps 0;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 eivltqspgtlsispgeratlsqcrasqisnlnhwqqkpgqprllikyasqsigp 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 61 RFGSGSGDTFTLTISLEPEDFAVYYCQSGSWPHFTFGGKTVEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 rfsgsgsgdtftltisrlepedfavyycqsgsnwphftfggktveik 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 6
AAB69678
ID AAB69678 standard; Protein; 107 AA.
XX
AC AAB69678;
XX
DT 30-APR-2001 (first entry)
XX
DE Humanised CMV5 antibody light chain SEQ ID NO: 63.
XX
KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
light chain; graft versus host disease; transplant; autoimmune disease;
multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
OS Mus sp.
XX
OS Homo sapiens.
XX
PN US6180370-B1.
XX
PD 30-JAN-2001.
XX
PF 07-JUN-1995; 95US-0484537.
XX
PR 28-DEC-1988; 88US-0290975.
PR 13-FEB-1989; 89US-0310252.
PR 28-SEP-1990; 90US-0590274.
PR 19-DEC-1990; 90US-0634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX
XX Producing humanized immunoglobulin, involves producing a cell
containing DNA segments encoding humanized heavy and light chain
variable regions, and expressing the DNA segments in the cell -
Disclosure; Fig 6; 145pp; English.
XX
XX The present invention describes a method of producing humanised
immunoglobulins involving expressing in a cell a nucleic acid encoding a
humanised version of an immunoglobulin. This is obtained by comparing a
donor and human immunoglobulin and producing a combined antibody which
contains part of each. These are useful in the treatment of
graft-versus-host disease, transplant rejection, autoimmune diseases such
as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
and systemic lupus erythematosus, herpes infections, CMV virus infections
and myeloid leukaemia. The present sequence is an antibody used to
demonstrate the method of the invention.
XX
SQ Sequence 107 AA;
Query Match 91.3%; Score 512; DB 22; Length 107;
Best Local Similarity 91.6%; Pred. No. 2e-32; 6; Indels 0; Gaps 0;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

OY 61 RFSGSGSCTDFLTITSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 rfsagsgtdftltisrlepedfavyycqsgnswphtfggkveik 107

RESULT 8

AAW84098
ID AAW84098 standard; Protein; 107 AA.
XX
AC AAW84098;
XX
DT 15-MAR-1999 (first entry)
XX
DE Humanised anti-alpha-v beta-3 MAB D12H2HC 1-0 VL.
XX
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12H2HC-10.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..97
FT /label= CDR3
XX
XX WO9840488-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US04987.
XX
XX 12-MAR-1997; 97US-0039609.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Johanson KO, Jonak ZL, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX
XX N-PSDB; AAV71800.
XX
XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX immunotherapeutic treatment of e.g. diabetic retinopathy,
XX inflammatory disorders, atherosclerosis, restenosis, cancers or
XX osteoporosis
XX
XX Claim 2; Page 61-62; 97pp; English.
XX
XX This is the amino acid sequence of the light chain variable region
XX (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
XX monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
XX (see AAW84096) of human Kabat subgroup III kappa chain, with
XX complementarity determining regions (CDRs) from the murine
XX anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
XX D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60)
XX are retained. The humanised light chain can be expressed in host
XX cells using nucleic acid molecules (see AAV71800) of the invention.
XX Humanised D12 VH is also provided (see AAW84097). The humanised
XX antibodies can be used for passive immunotherapy of disorders
XX mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
XX angiogenic-related disorders, such as angiogenesis associated
XX with diabetic retinopathy, atherosclerosis and restenosis, chronic
XX inflammatory disorders, macular degeneration, rheumatoid arthritis
XX and cancer, e.g. solid tumour metastasis, and diseases where bone
XX resorption is associated with pathology such as osteoporosis,
XX

CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC osteolytic lesions produced by bone metastasis, bone loss due to
CC immobilisation or sex hormone deficiency. They can also be used for
CC targeted drug therapy, and for detection and diagnosis.
XX
SQ Sequence 107 AA;

Query Match 90.9%; Score 510; DB 20; Length 107;
Best Local Similarity 90.7%; Pred No. 2.8e-32;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQISGIPA 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 1 divltqspgtlspsgeratlsqrasqisnhlhwqqkpgqaprlilikyasqisgips 60
OY 61 RFSGSGSCTDFLTITSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 rfsagsgtdftltisrlepedfavyycqsgnswphtfggkveik 107

RESULT 9

AAW84100
ID AAW84100 standard; Protein; 112 AA.
XX
AC AAW84100;
XX
DT 15-MAR-1999 (first entry)
XX
DE Vitronectin alpha-v beta-3 MAB VL.
XX
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
XX
OS Mus sp.
XX
XX WO9840488-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US04987.
XX
XX 12-MAR-1997; 97US-0039609.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Johanson KO, Jonak ZL, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX
XX N-PSDB; AAV71800.
XX
XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX immunotherapeutic treatment of e.g. diabetic retinopathy,
XX inflammatory disorders, atherosclerosis, restenosis, cancers or
XX osteoporosis
XX
XX Example 13; Page 64; 97pp; English.
XX
XX This is the amino acid sequence of the region of the murine
XX monoclonal antibody (MAB) D12 light chain variable region (VL)
XX that is altered in humanised D12 VL (see also AAW84096). A
XX synthetic gene (see AAV81902) encoding the protein was prepared
XX from synthetic oligonucleotides and used to prepare an expression
XX vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3
XX vitronectin receptor MAB. Humanised D12 MABs can be used for
XX passive immunotherapy of disorders mediated by the alpha-v beta-3
XX vitronectin receptor, e.g. restenosis and angiogenic associated
XX diseases.
XX

SQ Sequence 107 AA;

Query Match 89.3%; Score 501; DB 18; Length 107;
 Best Local Similarity 88.8%; Pred. NO. 1.3e-31;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQSLNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQSLNHLHWYQORPGQAPRLLIKYRSQISGIPA 60

OY 61 RFGSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107
 DB 61 RFGSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107

RESULT 12
 AAW08949
 ID AAW08949 standard; Protein; 107 AA.
 XX
 AC AAW08949;
 DT 18-SEP-1997 (first entry)
 XX
 DE Kappa light chain variable region of 225RB antibody.
 KW Kappa; light chain; reshaped; monoclonal; antibody; 225RB;
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KW tumour; cell; late stage; prostatic; prostate; variable region;
 KW framework; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..23 /label= framework_1
 FT Region 24..34 /label= CDR_1
 FT Region 35..49 /label= framework_2
 FT Region 50..56 /label= CDR_2
 FT Region 57..88 /label= framework_3
 FT Region 89..97 /label= CDR_3
 FT Region 98..107 /label= framework_4

WO9640210-A1.
 19-DEC-1996.
 07-JUN-1996; 96WO-US09847.
 15-DEC-1995; 95US-0573289.
 07-JUN-1995; 95US-0482982.
 (IMCL-) IMCLONE SYSTEMS INC.
 (MRCC-) MRC COLLABORATIVE CENT.
 Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;
 WPI; 1997-051897/05.
 Chimeric and humanised versions of anti-EGF receptor antibody 225 -
 used for inhibiting tumour growth, esp. of late stage prostatic
 tumour
 Claim 29; Fig 21; 112pp; English.
 The present sequence is the kappa light chain variable region
 of the reshaped human monoclonal antibody (MAB) H225, 225RKA. The

CC MAB is specific for the human epidermal growth factor (EGF)
 CC receptor.
 CC The MAB, or a fragment, can be used to inhibit the growth of tumour
 CC cells, especially late stage prostatic tumour cells in humans,
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle
 CC inhibitor.
 XX Sequence 107 AA;

Query Match 88.1%; Score 494; DB 18; Length 107;
 Best Local Similarity 87.9%; Pred. NO. 4.6e-31;
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQSLNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQSLNHLHWYQORPGQAPRLLIKYRSQISGIPA 60

OY 61 RFGSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107
 DB 61 RFGSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107

RESULT 13
 AAY32407
 ID AAY32407 standard; Protein; 127 AA.
 XX
 AC AAY32407;
 DT 13-MAR-2000 (first entry)
 XX
 DE Mouse anti-verotoxin II antibody VTml-1 humanised VL region.
 KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
 KW monoclonal antibody; light chain; mouse; humanised antibody; human;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 XX HUS; therapy.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..20 /note= "signal peptide"
 FT Protein 21..127 /note= "mature protein"
 FT Region 44..54 /note= "complementarity determining region 1"
 FT Region 70..76 /note= "complementarity determining region 2"
 FT Region 109..117 /note= "complementarity determining region 3"
 XX
 PN WO9959629-A1.
 PD 25-NOV-1999.
 PF 19-MAY-1999; 99WO-US11179.
 PR 20-MAY-1998; 98US-0086570.
 PA (TEIJ) TEIJIN LTD.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
 XX WPI; 2000-086580/07.
 DR N-PSDB; AAZ35244.
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli -

Claim 26: page 33-34: 77pp: English

The present sequence represents the variable light chain of humanised antibody L3.17. The antibody is effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases, and transplantation.

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Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
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Db
1 eivltaspatlsispqeratls crasqsisdylhwvqakpqaprllyvashsisqipa 60

61 RFSSGSGGDTFTLTISSEPEDFAVYCCQSGSWPHTFGGKTVEIK 107

Db 61 rfs gsgsgtdftlttisslepedfavycqhghsypwtfgggtkveik 107

RESOL 13
AAY30203

1D AA150203 standard, protein; 107 AA.
XX
XX

DT 01-NOV-

The variable light chain of human is

KW Light cha

KW collagen induced arthritis
KW collagen induced arthritis

KW I cell mediated disorder; autoimmune disease; HIV
transplantation.

XX	Synthetic.
OS	Homo sapiens.
OS	Homo sapiens.
XX	
PN	W09942075-A2.
XX	

XX
XX
JUN 07 07

10-FEB-1999:

XX

PR 19-FEB-1998;

XX

PA (BRIM) BRIST
YY

Aruffo AA. B

PI Huse WD, Siad

XX XX

DR WPI; 1999-5277
DR N-DCDR: 31310

XX
XX N-PSDB; AAZL10

Antibody that

PT disorders

XX

PS
XX
Claim 21; pag

The present s

CC antibody F4.

CC response again

CC and transplan

CC anti-inflammatory properties. The antibodies have wide therapeutic
CC applications, including autoimmune and inflammatory diseases and
CC transplantation. The antibody can be used in a pharmaceutical composition
CC for treating a patient suffering from a T cell mediated disorder. They
CC can also be used to treat autoimmune diseases, inflammatory diseases,
CC and transplantation.

XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 488; DB 20; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.3e-30;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGOAPRLIKYRSQISGIPA 60

DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGOAPRLIKYRSQISGIPA 60

QY 61 RFSGSGGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

DB 61 RFSGSGGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

Search completed: October 11, 2001, 12:01:58
Job time: 968 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:06 ; Search time 25.17 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-08-791-391A-4
Perfect score: 561
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWHPFGGKVKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PT05_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	91.3	107	1	US-07-634-278-63
2	512	91.3	107	1	US-07-634-278-87
3	512	91.3	107	1	US-08-477-728-63
4	512	91.3	107	1	US-08-477-728-87
5	512	91.3	107	1	US-08-474-040-63
6	512	91.3	107	1	US-08-474-040-87
7	512	91.3	107	1	US-08-487-200-63
8	512	91.3	107	1	US-08-487-200-87
9	512	91.3	107	4	US-08-484-537-63
10	512	91.3	107	4	US-08-484-537-87
11	486	86.6	127	2	US-08-476-176B-10
12	486	86.6	127	3	US-08-127-721A-10
13	486	86.6	127	3	US-08-485-246A-10
14	480	85.6	127	2	US-08-476-176B-6
15	480	85.6	127	3	US-08-127-721A-6
16	480	85.6	127	3	US-08-485-246A-6
17	479	85.4	107	2	US-08-232-081B-9
18	477	85.0	127	2	US-08-476-176B-8
19	477	85.0	127	3	US-08-127-721A-8
20	477	85.0	127	3	US-08-485-246A-8
21	448.5	79.9	107	3	US-08-783-853A-44
22	447	79.7	107	1	US-07-634-278-62
23	447	79.7	107	1	US-08-477-728-62
24	447	79.7	107	1	US-08-474-040-62
25	447	79.7	107	1	US-08-487-200-62
26	447	79.7	107	4	US-08-484-537-62
27	447	79.7	127	1	US-07-634-278-83

28 447 79.7 127 1 US-08-477-728-83 Sequence 83, Appl
29 447 79.7 127 1 US-08-474-040-83 Sequence 83, Appl
30 447 79.7 127 1 US-08-487-200-83 Sequence 83, Appl
31 447 79.7 127 4 US-08-484-537-83 Sequence 83, Appl
32 444 79.1 127 1 US-08-436-463-4 Sequence 4, Appl
33 440 78.4 107 1 US-08-436-463-20 Sequence 20, Appl
34 440 78.4 109 1 US-07-942-245-4 Sequence 1, Appl
35 437 77.9 107 1 US-08-107-669D-1 Sequence 1, Appl
36 437 77.9 107 1 US-08-472-788A-1 Sequence 1, Appl
37 437 77.9 107 2 US-08-477-531B-1 Sequence 1, Appl
38 437 77.9 107 2 US-08-082-842A-1 Sequence 1, Appl
39 436 77.7 111 1 US-07-634-278-47 Sequence 47, Appl
40 436 77.7 111 1 US-08-477-728-47 Sequence 47, Appl
41 436 77.7 111 1 US-08-474-040-47 Sequence 47, Appl
42 436 77.7 111 1 US-08-487-200-47 Sequence 47, Appl
43 436 77.7 111 4 US-08-484-537-47 Sequence 47, Appl
44 431.5 76.9 107 3 US-08-783-853A-57 Sequence 57, Appl
45 429.5 76.6 108 2 US-08-232-081B-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 91.3%; Score 512; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTSPATLSLSPGERATLSQASOSISNHLHWYQORPGQAPRLLIKYRSOSISGIPA 60
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Db 1 EIVLTSPGTLSPGERATLSQASOSISNHLHWYQORPGQAPRLLIKYRSOSISGIPD 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 RFSGSGGDTFTLTISLPEDEFAVYCCQSGSWPHTFGGTRKEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 RFSGSGGDTFTLTISLPEDEFAVYCCQSGSWPHTFGGTRKEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 2
US-07-634-278-87
; Sequence 87, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION DATA:
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 91.3%; Score 512; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTSPATLSLSPGERATLSQASOSISNHLHWYQORPGQAPRLLIKYRSOSISGIPA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 EIVLTSPGTLSPGERATLSQASOSISNHLHWYQORPGQAPRLLIKYRSOSISGIPD 60
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QY 61 RFSGSGGDTFTLTISLPEDEFAVYCCQSGSWPHTFGGTRKEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 RFSGSGGDTFTLTISLPEDEFAVYCCQSGSWPHTFGGTRKEIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 3
US-08-477-728-63
; Sequence 63, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 91.3%; Score 512; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTSPATLSLSPGERATLSQASOSISNHLHWYQORPGQAPRLLIKYRSOSISGIPA 60

Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60
QY 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107
Db 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107

RESULT 4
US-08-477-728-87
; Sequence 87, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 91.3%; Score 512; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60
QY 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107

Db 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107
RESULT 5
US-08-474-040-63
; Sequence 63, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 91.3%; Score 512; DB 1; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60
QY 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107
Db 61 RFGSGSGDTFTLTSSLEPEDFAVYVCOQSNWPHFTGGGKVEIK 107

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,200
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 87:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-487-200-87

Query Match 91.3%; Score 512; DB 1; Length 107;
 Best Local Similarity 91.6%; Pred. No. 5.6e-42;
 Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIKYSQISGIPD 60
 Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107
 Db 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107

RESULT 9
 US-08-484-537-63
 ; Sequence 63, Application US/08484537
 ; Patent No. 6180370
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,537
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-484-537-63

Query Match 91.3%; Score 512; DB 4; Length 107;
 Best Local Similarity 91.6%; Pred. No. 5.6e-42;
 Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60
 Db 1 EIVLTQSPGTLSLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIKYSQISGIPD 60
 Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107
 Db 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107

RESULT 10
 US-08-484-537-87
 ; Sequence 87, Application US/08484537
 ; Patent No. 6180370
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.

STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-10

Query Match 91.3%; Score 512; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 5.6e-42;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Sequence ID: Application US/08127121A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saidanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:

REFERENCE: NO. 6066718artis Patent and Trademark Department
ADDRESS: 59 Route 10
STREET: East Hanover
CITY: New Jersey
STATE: USA
COUNTRY: 07936-1080
ZIP: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127.721A

; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-127-721A-10

Query Match 85.6%; Score 486; DB 3; Length 127;
Best Local Similarity 86.0%; Pred. No. 2e-39;
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQISGITHYQKPGQAPRLLIKYASESISGIPS 80
Qy 61 RFSGSGGTDTLTISLLEPEDFAVYQCQSGSWPHTFGGKVEIK 107
Db 81 RFSGSGGTDTLTISRLEPEDFAMVYCCQSDSWPTTFGGTKVEIK 127

RESULT 13
US-08-485-246A-10
; Sequence 10, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Reshaped monoclonal isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,246A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6072035ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-246A-10

Query Match 86.6%; Score 486; DB 3; Length 127;
Best Local Similarity 86.0%; Pred. No. 2e-39;
Matches 92; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQISGITHYQKPGQAPRLLIKYASESISGIPS 80
Qy 61 RFSGSGGTDTLTISLLEPEDFAVYQCQSGSWPHTFGGKVEIK 107
Db 81 RFSGSGGTDTLTISRLEPEDFAMVYCCQSDSWPTTFGGTKVEIK 127

RESULT 14
US-08-476-176B-6
; Sequence 6, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-176B-6

Query Match 85.6%; Score 480; DB 2; Length 127;
Best Local Similarity 84.1%; Pred. No. 7.4e-39;
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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Db 21 DILLTQSPGTLSPGERATLSCRASQSIGTNIHWYQKPCQAPRLLIKYSSESIGIPS 80
QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKVEIK 107
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Db 81 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSDSWPTTFGGKVEIK 127

RESULT 15

US-08-127-721A-6
; Sequence 6, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-6

Query Match 85.6%; Score 480; DB 3; Length 127;
Best Local Similarity 84.1%; Pred. No. 7.4e-39;
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSIHNLHWYQORPCQAPRLLIKYSQISGIPA 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 21 DILLTQSPGTLSPGERATLSCRASQSIGTNIHWYQKPCQAPRLLIKYSSESIGIPS 80
QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKVEIK 107
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Db 81 RFGSGSGTDFTLTISLSEPEDFAVYCCQSGSDSWPTTFGGKVEIK 127

Search completed: October 11, 2001, 12:01:06
Job time: 916 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:31 ; Search time 2122.65 Seconds
(without alignments)
2557.737 Million cell updates/sec

Title: US-08-791-391A-5
Perfect score: 351
Sequence: 1 GAAGGCGACGTGGTGAGTC.....CTCTGGTCACGTCTCTGTGA 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: em_bal:*

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18: em_fun:*

19: em_htgo_hum:*

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22: em_htg_hum1:*

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90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

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97: gb_rod4:*

98: em_bal3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	309.4	88.1	482	10 I08289	I08289 Sequence 6
3	309.4	88.1	488	95 S45356	S45356 immunoglobu
4	302.2	86.1	351	9 AX060780	AX060780 Sequence
5	296.6	84.5	413	9 A38870	A38870 Sequence 24
6	295	84.0	413	9 AR013776	AR013776 Sequence
7	294.8	84.0	354	94 MUSIGMUD2A	M83724 Mouse monoc
8	293.6	83.6	721	9 AR027762	AR027762 Sequence


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Db 372 CTGCAAAATGACAGCTCTGAAGTCTGAGGACACAGCCGTGTATTACTGTGCAAGAGGTAC 431
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Db 432 GGCCTCCCTTTTGTCTACTGGGGCAAGGACTCTGGTCACTGCTCTGCA 482
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RESULT 3
LOCUS S45356 488 bp mRNA ROD 08-MAY-1993
DEFINITION immunoglobulin heavy chain variable-anti-human IL-2R [mice, mRNA
ACCESSION S45356
VERSION S45356.1 GI:255660
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 488)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J.,
Shedd,D., Cahill,K. and Zerler,B.
JOURNAL Differential effects of a murine and chimeric mouse/human
MEDLINE anti-interleukin-2 receptor antibody on human T-cell proliferation
REMARK Immunology 76 (3), 452-459 (1992)
92406249
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 115041] from the original journal article.
This sequence comes from Fig. 1b.
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/db_xref="taxon:10095"
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CDS
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/note="immunoglobulin heavy chain variable"
/note="anti-human IL-2R; This sequence comes from Fig. 1b"
/product="immunoglobulin heavy chain variable"
/protein_id="AAB23305.1"
/db_xref="GI:255661"
/translation="MNPGLRLFLVLTGKVEQVLESGGLVKPGSLKLSCAAS
GFAPSSIDMSVROTPEKRLWVAYISSGDNTYPTVKGRTISRDNKNTLYLQM
SSLKSEDTAVYYCARYGLPFPYWGQGLTVTSA"
BASE COUNT 114 a 116 c 132 g 126 t
ORIGIN

Query Match 88.1%; Score 309.4; DB 95; Length 488;
Best Local Similarity 92.6%; Pred. No. 4e-95;
Matches 325; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GAAGTGACGCTGTGGAGCTCTGGGGAGGCTTACTGAGCCCTGGAAGCTCCCTGAGACTC 60
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Db 137 GAAGTGACGCTGTGGAGCTCTGGGGAGGCTTACTGAGCCCTGGAAGCTCCCTGAAACTC 196
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Qy 61 TCCTGTGAGGCTCTGGATTGCTTTCAGTAGCTATGACATGCTCTTGGGTTTCGCCAGATT 120
|||
Db 197 TCCTGTGAGGCTCTGGATTGCTTTCAGTAGCTATGACATGCTCTTGGGTTTCGCCAGACT 256
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Qy 121 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTAGTGTGGTGGTAGCACTACTAT 180
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Db 257 CCGGAGAGAGGCTGGAGTGGTGCATACATTTAGTAGTGTGGTGGTAGCACTACTAT 316
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Qy 181 TTAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
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Db 317 CCAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAATGCCAAGAACCCCTTTAC 376
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Qy 241 CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
|||
Db 377 CTGCAAAATGACAGCTCTGAAGTCTGAGGACACAGCCGTGTATTACTGTGCAAGAGGTAC 436
|||
Qy 301 TACGCCAGTTTGTCTACTGGGGCAAGGACTCTGGTCACTGCTCTGCA 351
|||
Db 437 GGCCTCCCTTTTGTCTACTGGGGCAAGGACTCTGGTCACTGCTCTGCA 487
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RESULT 4
LOCUS AX060780 351 bp DNA PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078815.
ACCESSION AX060780
VERSION AX060780.1 GI:12406160
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 351)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
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Best Local Similarity 91.9%; Pred. No. 1.1e-92;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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RESULT 5
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ORIGIN

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 Best Local Similarity 90.0%; Pred. No. 3.5e-90;
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RESULT 7

MUSIGMUD2A

LOCUS MUSIGMUD2A 354 bp mRNA ROD 08-MAY-2000

DEFINITION Mouse monoclonal antiidiotypic antibody Igm VDJ-region mRNA.

ACCESSION M83724

VERSION M83724.1 GI:197951

KEYWORDS D-region; Ig heavy chain; J-region; V-region; immunoglobulin; immunoglobulin mu-chain; monoclonal antiidiotypic antibody.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 354)

AUTHORS Taub,R., Hsu,J.C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and Kohn,L.D.

TITLE Peptide sequences from the hypervariable regions of two monoclonal anti-idiotypic antibodies against the thyrotropin (TSH) receptor are similar to TSH and inhibit TSH-increased cAMP production in FRTL-5 thyroid cells

JOURNAL J. Biol. Chem. 267 (9), 5977-5984 (1992)

MEDLINE 92210565

FEATURES

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Best Local Similarity 91.5%; Pred. No. 4e-90;
Matches 324; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
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RESULT 8
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LOCUS          AR027762      721 bp      DNA
DEFINITION    Sequence 15 from patent US 5856456.
ACCESSION     AR027762
VERSION       AR027762.1 GI:5938582
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 721)
AUTHORS       Whitlow,M.D. and Filpula,D.R.
TITLE         Linker for linked fusion polypeptides
JOURNAL       Patent: US 5856456-A 15 05-JAN-1999;
FEATURES      Location/Qualifiers
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BASE COUNT    176 a      172 c      189 g      184 t
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Query Match    83.6%; Score 293.6; DB 9; Length 721;
Best Local Similarity 90.2%; Pred. No. 1.1e-89;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTCCCTGAGACTC 60
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RESULT 10
AR027763
LOCUS          AR027763      733 bp      DNA
DEFINITION    Sequence 17 from patent US 5856456.
ACCESSION     AR027763
VERSION       AR027763.1 GI:5938583
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
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RESULT 9
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LOCUS          AR088763      721 bp      DNA
DEFINITION    Sequence 15 from patent US 5990275.
ACCESSION     AR088763
VERSION       AR088763.1 GI:10015526
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 721)
AUTHORS       Whitlow,M.D. and Filpula,D.R.
TITLE         Linker and linked fusion polypeptides
JOURNAL       Patent: US 5990275-A 15 23-NOV-1999;
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BASE COUNT    176 a      172 c      189 g      184 t
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Query Match    83.6%; Score 293.6; DB 9; Length 721;
Best Local Similarity 90.2%; Pred. No. 1.1e-89;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTCCCTGAGACTC 60
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Db 364 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTCCCTGAAACTC 423
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RESULT 10
AR027763
LOCUS          AR027763      733 bp      DNA
DEFINITION    Sequence 17 from patent US 5856456.
ACCESSION     AR027763
VERSION       AR027763.1 GI:5938583
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
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Db 61 TCCTGTGCAGCCTCTGGATTCACCTTTCAGTAGCTATACCATGCTCTTGGTTGCCAGACT 120
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RESULT 13
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LOCUS Mus musculus hybridoma Y6-8G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113107
VERSION AF113107.1 GI:4768654
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 354)
AUTHORS Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J.,
Jennette,J.C. and Nachman,P.H.
TITLE Restriction in Vkappa gene use and antigen selection in
anti-myeloperoxidase response in mice
JOURNAL J. Immunol. 165 (7), 3890-3897 (2000)
MEDLINE 20487209
REFERENCE 2 (bases 1 to 354)
AUTHORS Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., Kinjoh,K.,
Tuttle,R. and Taylor,J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
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BASE COUNT 84 a 80 c 102 g 88 t
ORIGIN

Query Match 82.6%; Score 290; DB 94; Length 354;
Best Local Similarity 90.7%; Pred. No. 1.8e-88;
Matches 321; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
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Db 241 CTGCAAAATGAGCAGTCTGAATCTCTGAGGACACAGCCATGTATTACTGTGCAAGAGGTTAC 300
QY 301 TACGG---CAGTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351
Db 301 TATAGTAACTACTTTGCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 354

RESULT 14
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LOCUS Mus musculus hybridoma Y6-9G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113108
VERSION AF113108.1 GI:4768656
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 354)
AUTHORS Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J.,
Jennette,J.C. and Nachman,P.H.
TITLE Restriction in Vkappa gene use and antigen selection in
anti-myeloperoxidase response in mice
JOURNAL J. Immunol. 165 (7), 3890-3897 (2000)
MEDLINE 20487209
REFERENCE 2 (bases 1 to 354)
AUTHORS Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., Kinjoh,K.,
Tuttle,R. and Taylor,J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
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NYFAYWGQGLTVTSA"
BASE COUNT 84 a 80 c 102 g 88 t
ORIGIN

Query Match 82.6%; Score 290; DB 94; Length 354;
Best Local Similarity 90.7%; Pred. No. 1.8e-88;
Matches 321; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
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QY 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGTAGCAGCTACTAT 180
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QY 301 TACGG---CAGTTTTCCTACTGGGCGCAAGGAGCTCTGCTACTGCTCTGCA 351
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Db 301 TATAGTAACACTACTTTGCTTACTGGGCGCAAGGAGCTCTGGTCACTGCTCTGCA 354
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RESULT 15
MUSIGHNRZ
LOCUS MUSIGHNRZ 350 bp mRNA ROD 23-SEP-1994
DEFINITION Mus musculus Igh chain A allele of At8-1-12 mRNA, VDJ region.
ACCESSION M28187
VERSION M28187.1 GI:548170
KEYWORDS D-segment; J-segment; V-region; V-segment; immunoglobulin;
immunoglobulin heavy chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) newborn cdna
to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 350)
AUTHORS Komori,T., Sugiyama,H. and Kishimoto,S.
TITLE A novel V-H-DJ-H to J-H joining that induces H chain production in
an Ig-null immature B cell line
JOURNAL J. Immunol. 143, 1040-1045 (1989)
MEDLINE 89309739
COMMENT On Sep 24, 1994 this sequence version replaced gi:341843.
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CDS
CDS
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Search completed: October 11, 2001, 15:09:32
Job time: 6354 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:34:02 ; Search time 2341.88 Seconds
 (without alignments)
 1416.790 Million cell updates/sec

Title: US-08-791-391A-5
Perfect score: 351
Sequence: 1 GAAGTCACAGCTGGTGAGTC.....CTCTGCTCACTGCTCTGCA 351

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.4	79.0	877	145	BF144493
2	266.4	75.9	1559	145	BF138708
3	260.8	74.3	494	174	BG145342
4	258.6	73.7	404	149	BF452207
5	258.6	73.7	469	23	AL645111
6	258.6	73.7	823	3	AF170256
7	255.8	72.9	886	150	BF582912
8	255	72.6	1012	145	BF142302
9	254.8	72.6	774	150	BF581450
10	254.2	72.4	662	145	BF163874
11	252.6	72.0	650	150	BF579001
12	252.4	71.9	904	145	BF180238
13	251	71.5	913	145	BF162056
14	250.2	71.3	454	121	AW824857
15	244	69.5	862	145	BF143948
16	243.2	69.3	908	145	BF161883
17	243	69.2	718	145	BF136279
18	241.2	68.7	689	150	BF579926
19	240.8	68.6	987	150	BF577496
20	240.4	68.5	940	150	BF580726
21	231.6	66.0	415	113	AW215320
22	231.4	65.9	677	165	BE286624
23	230	65.5	406	115	AW401971
24	229.4	65.4	969	150	BF579260
25	226.2	64.4	511	115	AW402613
26	219.2	62.5	415	9	AA575218
27	219.2	62.5	456	115	AW403059
28	218.2	62.2	440	115	AW408304
29	218	62.1	582	115	AW401386
30	217.6	62.0	1164	172	BF974771
31	216.8	61.8	548	115	AW408295
32	215.8	61.5	991	172	BF974524
33	215.6	61.4	735	106	AL551886
34	215.4	61.4	471	115	AW403220
35	215.2	61.3	964	151	BF663281
36	215	61.3	648	132	BG340670
37	214.2	61.0	678	152	BG340648
38	213.6	60.9	491	115	AW402907
39	212.4	60.5	436	115	AW402311
40	212.2	60.5	687	153	BG397964
41	210.8	60.1	487	115	AW403862
42	210.2	59.9	447	115	AW402793
43	210.2	59.9	510	115	AW403707
44	210	59.8	396	115	AW407843
45	209.2	59.6	518	115	AW402029

ALIGNMENTS

RESULT	1
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DEFINITION	BF01790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5', mRNA sequence.
ACCESSION	BF144493
VERSION	BF144493.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 877)
TITLE	NIH-MGC http://mgi.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

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1..877	found through the I.M.A.G.E. Consortium/LLNL at:
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1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
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1..877	/tissue_type="tumor, metastatic to mammary"
1..877	/clone_lib="NCI_CGAP_Lu30"
1..877	/db_xref="taxon:10090"
1..877	/strain="C57BL/6J"
1..877	/organism="Mus musculus"
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1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
1..877	/lab_host="DH10B"
1..877	/tissue_type="tumor, metastatic to mammary"
1..877	/clone_lib="NCI_CGAP_Lu30"
1..877	/db_xref="taxon:10090"
1..877	/strain="C57BL/6J"
1..877	/organism="Mus musculus"
1..877	1. 877
1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
1..877	/lab_host="DH10B"
1..877	/tissue_type="tumor, metastatic to mammary"
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1..877	/organism="Mus musculus"
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1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
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1..877	/tissue_type="tumor, metastatic to mammary"
1..877	/clone_lib="NCI_CGAP_Lu30"
1..877	/db_xref="taxon:10090"
1..877	/strain="C57BL/6J"
1..877	/organism="Mus musculus"
1..877	1. 877
1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
1..877	/lab_host="DH10B"
1..877	/tissue_type="tumor, metastatic to mammary"
1..877	/clone_lib="NCI_CGAP_Lu30"
1..877	/db_xref="taxon:10090"
1..877	/strain="C57BL/6J"
1..877	/organism="Mus musculus"
1..877	1. 877
1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
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1..877	/tissue_type="tumor, metastatic to mammary"
1..877	/clone_lib="NCI_CGAP_Lu30"
1..877	/db_xref="taxon:10090"
1..877	/strain="C57BL/6J"
1..877	/organism="Mus musculus"
1..877	1. 877
1..877	Location/Qualifiers
1..877	High quality sequence stop: 644.
1..877	Plate: LAM9275 row: a column: 10
1..877	http://image.llnl.gov
1..877	found through the I.M.A.G.E. Consortium/LLNL at:
1..877	Clone distribution: NCI-CGAP clone distribution information can be
1..877	DNA Sequencing by: InCyte Genomics, Inc.
1..877	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1..877	Tissue Procurement: Gilbert Smith, Ph.D.
1..877	Email: cgapbs-r@mail.nih.gov
1..877	Investigator providing samples: Gilbert Smith, NIH
1..877	dt. Library constructed by Life Technologies.
1..877	MWV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1..877	Site 2: Salt; transgenic model WNT-1, expression driven by
1..877	/note

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLN9246 row: j column: 24
High quality sequence stop: 562.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 404)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1436665
Seq primer: -40RP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
1. 404
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3675897"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 96 a 94 c 109 g 105 t
ORIGIN

Query Match 73.7%; Score 258.6; DB 149; Length 404;
Best Local Similarity 91.9%; Pred. No. 2.4e-69;
Matches 273; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCTCGAGACTC 60
|||||
Db 106 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCTCGAGACTC 165
|||||
QY 61 TCCTGTGCAGCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120
|||||
Db 166 TCCTGTGCAGCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 225
|||||
QY 121 CCGGAGAAGAGGCTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
|||||
Db 226 CCGGAAAAGAGGCTGGAGTGGTGCAGCAACCATTAGTAGTGGTGGTTACCACTACTAT 285
|||||
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
|||||
Db 286 CTAGACAGTGTGAAGGTCGATTACCATCTCCAGAGACAATGCCAAGAACCCCTGTAC 345
|||||
QY 241 CTGCAATGACGAGTGAACCTCTGAGGACACAGCCATGTATTACTGTCCAGAGAT 297
|||||
Db 346 CTGCAATGACGAGTGTAGGCTCTGAGGACACAGCCATGTATTACTGTCCAGAGAT 402
|||||

RESULT 5
AI645111 469 bp mRNA EST 15-MAR-2000
LOCUS ms87g10.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:618594
DEFINITION 5', similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U23089 Mus musculus CB17 SCID Immunoglobulin heavy
chain V region mRNA, (MOUSE);, mRNA sequence.
ACCESSION AI645111
VERSION AI645111.1 GI:4723586
KEYWORDS EST.
SOURCE house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 469)
Marra.M., Hillier.L., Kucaba.T., Martin.J., Beck.C., Wylie.T.,
Underwood.K., Steptoe.M., Theising.B., Allen.M., Bowers.Y., Person
B., Swaller.T., Gibbons.M., Pape.D., Harvey.N., Schurk.R., Ritter
E., Kohn.S., Shin.T., Jackson.Y., Cardenas.M., McCann.R.,
Waterston.R. and Wilson.R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MGI:379418
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 469
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:618594"
/clone_lib="Soares mouse 3NDMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTACCAATCTGAAGTGGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 112 c 121 g 123 t
ORIGIN

Query Match 73.7%; Score 258.6; DB 23; Length 469;
Best Local Similarity 91.9%; Pred. No. 2.5e-69;
Matches 273; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCTCGAGACTC 60
|||||
Db 118 GAGGTGAAGCTGGTGGAGTCTGGGAAAGCTTAGTGAAGCCTGGAGGTCCTCGAGACTC 177
|||||
QY 61 TCCTGTGCAGCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120
|||||
Db 178 TCCTGTGCAGCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 237
|||||
QY 121 CCGGAGAAGAGGCTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
|||||
Db 238 CAGAGAAGAGGCTGGAGTGGTGCAGATACATAGTAGTGGTGGTAGTACTACTAT 297
|||||
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
|||||
Db 298 GCAGACACTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACCCCTGTAC 357
|||||
QY 241 CTGCAATGACGAGTGAACCTCTGAGGACACAGCCATGTATTACTGTCCAGAGAT 297
|||||
Db 358 CTGCAATGACGAGTGTGAAGTCTGAGGACACAGCCATGTATTACTGTCAAGAGAT 414
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[illegible]

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QY 181 TTAGACACTGTGCAGGCGCGATTCCACATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
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Db 238 CCAGACAGTATGAAGGGCGGATTCCACATCTCCAGAGACAATGCCAAGAACACCCGTGTTA 297
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CTGCAATGAGCAGTCTGAACCTGTGAGGACACAGCCATGATTACTGTGCAAGACATAAC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 CTGCAATGAGCAGTCTGAATCTGTAGGACACAGCCGTGATTATTGTACAGAGGTGAC 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TAGCGCAGTTTTGCTTACTGGGCGCCAGGACTCTGTGCTCACTGCTCTC 347
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 TACTGTACTTCGATGCTGGGCGCGAGGACCACCGTCAACCGTCTC 404
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
LOCUS BF142302 1012 bp mRNA EST 24-OCT-2000
DEFINITION 601791844F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4022459 5',
    mRNA sequence.
ACCESSION BF142302
VERSION BF142302.1 GI:10981252
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1012)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9279 row: h column: 12
High quality sequence stop: 711.
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    /organism="Mus musculus"
    /strain="CZECH II"
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    /clone_lib="NCI_CGAP_Lu30"
    /tissue_type="tumor, metastatic to mammary"
    /lab_host="DH10B"
    /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: SalI; transgenic model WNT-1, expression driven by
    MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
    dt. Library constructed by Life Technologies.
    Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 273 a 271 c 267 g 201 t
ORIGIN
    Query Match 72.6%; Score 255; DB 145; Length 1012;
    Best Local Similarity 82.9%; Pred. No. 4e-68;
    Matches 291; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGTGAGTCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTCGAGACTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 101 GAGTGCACCTGTGTGAGTCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTCGGAACATC 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TCTGTGCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTTTGGGTTCCGCCAGATT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 TCCTGTGCAGCCTCTGGATTCACCTTTTCAGTAGCTATGGAATGCACTGGGTTCTGCAGGCT 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCGGAGAAGAGGCTGAGTGGGTGCGAAAAGTTAGTAGTGGTGGTACCACTACTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 CCAGAGAAGGGGCTGAGTGGGTGCGAATACATATAGTAGTGGCAGTAGTACCACTACTAT 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 181 TTAGACACTGTGCAGGCGCGATTCCACATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
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Db 281 GCAGACAGTGAAGGGCGGATTCCACATCTCCAGAGACAATGCCAAGAACACCCCTGTTTC 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CTGCAATGAGCAGTCTGAACCTGTGAGGACACAGCCATGATTACTGTGCAAGACATAAC 300
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Db 341 CTGCAATGAGCAGTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGGCGAGGT 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TAGCGCAGTTTTGCTTACTGGGCGCCAGGACTCTGTGCTCACTGCTCTGCA 351
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 401 TACTCCCTATGAGCTACTGGGGTCAAGGAACCTCAGTACCCGCTCTCTCA 451
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
LOCUS BF581450 774 bp mRNA EST 12-DEC-2000
DEFINITION 602100853F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224109 5',
    mRNA sequence.
ACCESSION BF581450
VERSION BF581450.1 GI:11655162
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 774)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9813 row: j column: 14
High quality sequence stop: 675.
FEATURES
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    /strain="FVB/N"
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    /clone_lib="NCI_CGAP_Co24"
    /lab_host="DH10B (T1 phage-resistant)"
    /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.6 Kb. Constructed by Life
    Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 191 a 200 c 201 g 182 t
ORIGIN
    Query Match 72.6%; Score 254.8; DB 150; Length 774;
    Best Local Similarity 90.9%; Pred. No. 4.3e-68;
    Matches 271; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGTGAGTCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTCGAGACTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 GAGTGCACCTGTGTGAGTCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTCGAATC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TCTGTGCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTTTGGGTTCCGCCAGATT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 TCCTGTGCAGCCTCTGGATTCATTTCAGTAGCTATGCGATGCTTTGGGTTCCGCCAGAT 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCGGAGAGAGGCTGAGTGGGTGCGAAAAGTTAGTAGTGGTGGTACCACTACTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 CCGGAGAAGGGCTGAGTGGGTGCGAGCCATTAATAGTAAGGGTGGGAGACCAACTAT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db	296	CTAGACATTATAAGGGCCGCGATTACCACATCTCCAGAGACAAATGTCAAGAACATCCTGTAT	355
Qy	241	CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCATGTATTACTGTGCAA---GACAT	297
Db	356	CTGCAAAATGACAGCTCTGAAGCTCTGAGGACACGCCACATATTACTGTGCAAGTGGAGAT	415
Qy	298	AACCTACGACAGTTTTCCTTACTTGGGGCAAGGACTCTGTCTACTGTCTCTGCA	351
Db	416	GATGACGCTGGTTGTCTTACTTGGGGCAAGGACTCTGGTCTACTGTCTCTGCA	469
RESULT 13			
BF162056 913 bp mRNA EST 30-OCT-2000			
LOCUS 601768714F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987986 5',			
DEFINITION mRNA sequence.			
ACCESSION BF162056			
VERSION BF162056.1 GI:11042257			
KEYWORDS EST.			
SOURCE house mouse.			
ORGANISM Mus musculus			
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE 1 (bases 1 to 913)			
JOURNAL NIH-MGC http://mgs.nci.nih.gov/.			
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-re@mail.nih.gov			
Tissue Procurement: Gilbert Smith, Ph.D.			
cDNA Library Preparation: Life Technologies, Inc.			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: L1AM9195 row: 1 column: 03			
High quality sequence stop: 581.			
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/strain="CZECH II (fetal)"			
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/clone="IMAGE:3987986"			
/clone_lib="NCI_CGAP_Lu29"			
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Stem cell origin."			
/lab_host="DH10B"			
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Salt;			
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.			
Library constructed by Life Technologies. Investigator			
providing samples: Gilbert Smith, NIH"			
BASE COUNT 218 a 246 c 260 g 187 t			
ORIGIN			
Query Match 71.5% Score 251; DB 145; Length 913;			
Best Local Similarity 85.3%; Pred. No. 6.7e-67;			
Matches 308; Conservative 0; Mismatches 40; Indels 13; Gaps 2;			
Qy	1	GAAGTGCAGCTGTGGAGCTCTGGGGAGGCTTACTGAAGCCTGGAAGGTCCCTGAGACTC	60
Db	127	GAAGTGCAGCTGTGGAGCTCTGGGGAACTTAGTGAAGCCTGGAGGTCCCTGAAACTC	186
Qy	61	TCCGTGTGAGCCTCTGGATTGCTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGATT	120
Db	187	TCCTGTGCAGCTTCTGGATTCACTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGACT	246
Qy	121	CCGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTAGCACCTACTAT	180
Db	247	CCGGAGAAGAGGCTGGAGTGGGTGCG---AGCCATTAGTGGTGGTAGCACCTACTAT	303
Qy	181	TTAGACACTGTGTCAGGGCCGATTACCATCTCCAGAGACAAATGCCAAGAACACCTCTATAC	240

Db 304 CCAGACAGTGTGAAGGGTCGATTACCATCTCCAGAGACAAGGCCAAGACACCTGTAC 363
QY 241 CTGCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGAC - - - - 295
Db 364 CTCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACGTGGT 423
QY 296 - - - - -ATAACTACGCGAGTGTGTTTCTACTGGGCGCAAGGACTCTGGTCACTGTCTCTGC 350
Db 424 GGTTACTACGATGGTACTTCCGATGTCTGGGCGCAGGACCACGGTCAACGCTCTCTC 483
QY 351 A 351
Db 484 A 484

RESULT 14
AW824857
LOCUS
DEFINITION
us08c01.y1 Soares_NMGBC_B-cell Mus musculus cDNA clone
IMAGE:3166464 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR
V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID
immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AW824857
AW824857.1 GI:7917934
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 454)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-re@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1061924
Seq primer: -40RP from Gibco.
FEATURES
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1..454
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/clone="IMAGE:3166464"
/clone_lib="Soares_NMGBC_B-cell"
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/lab_host="DH10B (phage resistant)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGCGCGCGAGGATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 102 a 109 c 127 g 116 t
ORIGIN
Query Match 71.3%; Score 250.2; DB 121; Length 454;
Best Local Similarity 85.1%; Pred. No. 9.9e-67;
Matches 292; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
QY 1 GAAGTCAGCTGTGGAGTCTGGGGAGGCTTAGTAGAGCTGGAAGGCTCCCTGAGACTC 60

Db 112 GAGCTGACGTGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGCTCCTGAAACTC 171
QY 61 TCCTGTGCAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120
Db 172 TCCTGTGCAGCCTCTGGATTCACCTTTCAGTGACTATGGAATGCACCTGGTTCGTCAGGCT 231
QY 121 CCGGAGAAGAGGCTGGAGTGGTCGCAAAAGCTTAGTAGTGGTGGTGGTAGCCACTACTAT 180
Db 232 CCAGAGAAGGCTGGAGTGGTGGTTCATACATTAGTAGTGCAGTAGTACCATTACTAT 291
QY 181 TTAGACACTGTGCAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
Db 292 GCAGACACAGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTGTC 351
QY 241 CTGCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGAC - - - AT 297
Db 352 CTGCAAAATGAGCAGTCTGAGGCTGAGGACACGCCCATGTATTACTGTGCAAGCCCGGG 411
QY 298 AACTACGCGCAGTTTGTCTACTGGGCGCAAGGACTCTGGTCA 340
Db 412 GGTTCCTCTGGTTGCTTACCTGGGCGCAAGGACTCTGGTCA 454

RESULT 15
BF143948
LOCUS
DEFINITION
601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BF143948
BF143948.1 GI:10982988
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 862)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9258 row: i column: 23
High quality sequence stop: 671.

FEATURES
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Location/Qualifiers
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/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4014430"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies."
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 213 a 236 c 236 g 176 t 1 others
ORIGIN

Query Match 69.5%; Score 244; DB 145; Length 862;
Best Local Similarity 82.7%; Pred. No. 9.7e-65;
Matches 291; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

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Db |||||||
QY 99 GAGGTGCACCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCCGGAACTC 158
Db |||||||
QY 61 TCCTGTGCAGCCTCTGGATTCTTCAGTAGCTATGACATGTCTTGGGTTCCCGCAGATT 120
Db |||||||
QY 159 TCCTGTGCAGCCTCTGGATTCTTCAGTAGCTATGGAATGCACTGGGTTGTCAGGCT 218
Db |||||||
QY 121 CCGGAGAGAGGCTGGAGTGGGTCCGAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
Db |||||||
QY 219 CCAGAGAGGGGCTGGAGTGGGTGGCATATAGTAGTGGCAGTAGTACCATCTACTAT 278
Db |||||||
QY 181 TTAGACTGTGCAGGCCGATTCCACATCTCCAGAGACAATCCCAAGAACACCCCTATAC 240
Db |||||||
QY 279 GCAGACACAGTGAAGGGCCGATTCCACATCTCCAGAGACAATCCCAAGAACACCCCTGTC 338
Db |||||||
QY 241 CTGCAAAATGACAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db |||||||
QY 339 CTGCAAAATGACAGTCTGAAGGCTCTGAGGACACGGCCATGTATTACTGTGCAAGGCCAGGT 398
Db |||||||
QY 301 TACGGCAGT-TTTGCTTACTGGGGCAAGGGACTCTGGTCACTGTCTCTGCA 351
Db |||||||
QY 399 TACTCCCTATCGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCA 450

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Job time: 5541 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:36 ; Search time 177.65 seconds
(without alignments)
1240.605 Million cell updates/sec

Title: US-08-791-391a-5

Perfect score: 351

Sequence: 1 GAAGTGCAGCTGGTGGAGTC.....CTCTGCTACTGCTCTGTGCA 351

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	351	100.0	351	19	AAV49822
2	351	100.0	351	22	AAV28177
3	309.4	88.1	482	11	AAQ05555
4	302.2	86.1	351	19	AAV49820
5	302.2	86.1	351	22	AAV28175
6	296.6	84.5	413	15	AAQ06850
7	293.6	83.6	721	20	AAV99765
8	293.6	83.6	721	21	AAV37397
9	293.6	83.6	733	20	AAV99766
10	293.6	83.6	733	21	AAV37398
11	291	82.9	369	19	AAV07642
					LM609 antibody hea
					Antibody LM609 hea
					Sequence encoding
					Vitaxin antibody h
					Vitaxin heavy chai
					MAB A33 heavy chai
					A33/212 single-cha
					Linked fusion prot
					A33/218 single-cha
					Linked fusion prot
					anti-CD22 monoclon

12	289.6	82.5	1938	19	AAV58929	A33 chimeric recep
13	284	80.9	418	15	AAQ62764	Murine KC-4 immuno
14	284	80.9	418	15	AAQ62789	Murine KC-4 immuno
15	283.6	80.8	411	19	AAV24232	Chimeric antibody
16	283.6	80.8	411	20	AAQ00092	Chimeric antibody
17	283.6	80.8	411	21	AAZ58913	Mouse humanised an
18	283.6	80.8	411	21	AAZ58913	Mouse antibody H c
19	283.6	80.8	411	22	AAV69129	Human pTHrp mouse
20	283.6	80.8	411	22	AAV69185	Human pTHrp mouse
21	282.4	80.5	441	22	AAV69241	Human pTHrp mouse
22	282.4	80.5	441	22	AAV72269	Chimeric MAB 15 PC
23	282.2	80.4	480	13	AAQ20070	MRK16-H chain. Ch
24	280.8	80.0	457	18	AAV72267	Mouse MAB 15 heavy
25	277.4	79.0	357	15	AAQ66409	VH coding region o
26	274.6	78.2	417	15	AAQ62804	Humanised murine K
27	271.6	77.4	351	16	AAQ87534	Humanised anti-KC-
28	271.6	77.4	351	16	AAQ62822	Human Ige receptor
29	271.6	77.4	351	16	AAQ62824	Human Ige receptor
30	271	77.2	445	14	AAQ36530	cDNA encoding heav
31	271	77.2	445	14	AAQ36537	Chimeric MAB heavy
32	271	77.2	491	14	AAQ36535	BR55-2 heavy chain
33	269.4	76.8	923	16	AAV51436	Murine MAB SK48-E2
34	268.8	76.6	324	13	AAQ20303	B cell hybridoma 1
35	268.6	76.5	426	14	AAQ34576	Antibody 4A2 heavy
36	267.8	76.3	357	19	AAV44997	15D3 antibody heav
37	267.8	76.3	357	20	AAZ10957	15D3 VH chain codi
38	267.8	76.3	357	20	AAV08933	Antibody 15D3 hea
39	266.2	75.8	357	16	AAV04997	Antibody 3S193 hea
40	266.2	75.8	357	17	AAV28000	B5 immunoglobulin
41	264.6	75.4	699	17	AAV16700	Lewis-Y antibody B
42	264.6	75.4	8327	19	AAV18597	Plasmid pD17-cj-dC
43	264.6	75.4	8691	19	AAV18696	Plasmid expressing
44	263.6	75.1	717	14	AAQ40463	Fv(TU25). Homo sa
45	263	74.9	357	17	AAV16699	Lewis-Y antibody B

ALIGNMENTS

RESULT 1

AAV49822 AAV49822 standard; DNA; 351 BP.

XX AC AAV49822;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody heavy chain variable region DNA fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.

XX OS Mus sp.

XX PH Key Location/Qualifiers
XX FT CDS 1..351
XX FT /*tag= a
XX FT /product= "LM609 antibody heavy chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX


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XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 75..482
XX FT /*tag= a
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XX PD 01-AUG-1990.
XX PF 24-JAN-1990; 90EP-0101351.
XX PR 04-DEC-1989; 89US-04411702.
XX PR 24-JAN-1989; 89US-0301216.
XX PA (MOLE-) MOLECULAR THERAPEU.
XX PI Zerler B;
XX WPI; 1990-232892/31.
XX P-PSDB; AAR06251.
XX Expression vectors for producing chimeric monoclonal antibodies -
XX PT which express human constant region and non-human variable region
XX PS Disclosure; ; P; English.
XX CC MAb's comprising mouse CH and CL constant regions which human
XX CC variable regions may be used to create mouse/human hybrid MAb's,
XX CC which have a longer serum half-life. Method can be used to produce
XX CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX SQ Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;

Query Match 88.1%; Score 309.4; DB 11; Length 482;
Best Local Similarity 92.6%; Pred. No. 1.2e-82;
Matches 325; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTAGTGAGCCTGGAAGCTGCGCTGAGACTC 60
DB 132 gaagtcagctgtggagctggggaggttagtgagcctggaagctgaggtccctgaaactc 191
QY 61 TCCTGTGACGCTGTGATTCGCTTTCAGTAGCTATGACATGCTGTGCTGCGCAGATT 120
DB 192 tctgtgacgctgtgattcgcttcttcagtagcattgacatgcttctgggtcgccagact 251
QY 121 CCGGAGAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTGGTACTACTAT 180
DB 252 ccggagaagagctggagtggtgctgcatacattagtagtggtggtgatacacctactat 311
QY 181 TTAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACATGCCAAGACACCCCTATAC 240
DB 312 ccagacactgtgaaggccgagctcattccattccagagacatgccaagaacaccccttac 371
QY 241 CTGCAATGAGCAGCTGGAAGCTCTGAGGACACAGCCATGATTACTGTGCAAGACATAAC 300
DB 372 ctgcaaatgagcagctggaagctctgagacacagccgtgattactgtgcaagaaggtac 431
QY 301 TAGCGGAGTTTGTACTGGGCGCAAGGACTGTGCTACTGTCTGTGCA 351
DB 432 ggctcccttctgcttactgggccaaggagactctgctgctctgca 482

RESULT 4
AAV49820
ID AAV49820 standard; DNA; 351 BP.
XX AC AAV49820;
XX DT 02-NOV-1998 (first entry)
XX

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DE XX Vitaxin antibody heavy chain variable region DNA.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 1..351
XX FT /*tag= a
XX FT /product= "vitaxin antibody heavy chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"
XX PN W09833919-A2.
XX XX
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI; 1998-437472/37.
XX DR P-PSDB; AAW76001.
XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX PS Claim 3; Fig 1a; 129pp; English.
XX CC This sequence encodes the vitaxin antibody variable heavy chain region.
XX CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
XX CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX CC block integrin-mediated signal transduction. This is useful in the
XX CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 86.1%; Score 302.2; DB 19; Length 351;
Best Local Similarity 91.9%; Pred. No. 1.5e-80;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AAGTGCAGCTGTGGAGCTGGGGAGGCTTAGTGAGCCTGGAAGCTGCGCTGAGACTCT 61
DB 2 aggtgcagctgtggagctggggaggttagtgagcctggaagctgagactct 61
QY 62 CCTGTGACGCTCTGGATTTCGCTTTTCAGTAGCTATGACATGCTTTGGTTCCGCGAGATT 121
DB 62 cctgtgacgctctggatttcgcttttcagtagctatgacatgctttggttccgagactc 121
QY 122 CGGAGAAAGAGCTGGAGTGGGTGCGAAAGTTAGTGGTGGTGGTAGCCACTTATT 181
DB 122 cgggaaagagctggagtggttcgaaaagttagtggtgggttagcaccctactatt 181
QY 182 TAGACACTGTGACAGGCGGCGATTTCACCATCTCCAGAGACATGCCAAGACACCCCTATAC 241
DB 182 tagacactgtgacaggcggttcaccatctccagagacaatagtagaagacacccctatacc 241

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QY 242 TGCAGTACGAGCTGTAAGTCTGAGGACACAGCCAGTATTACTGTGCAAGACATAACT 301
 Db 242 TGCAGTACGAGCTGTAAGTCTGAGGACACAGCCAGTATTACTGTGCAAGACATAACT 301
 QY 302 ACGGAGTATTTGCTTACTGGGCCAAGGAGGACTGTGTCATCTCTCT 348
 Db 302 ACGGAGTATTTGCTTACTGGGCCAAGGAGGACTGTGTCATCTCTCT 348

RESULT 5
 AAF28175 standard: DNA; 351 BP.
 AC AAF28175;
 DT 03-APR-2001 (first entry)
 DE Vitaxin heavy chain variable region DNA.
 KW LM609; grafted antibody; alphaVbeta₃ integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
 OS Unidentified.
 XX
 PN WO200078815-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000WO-US17454.
 XX
 PR 24-JUN-1999; 99US-0339922.
 XX
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
 XX
 PI Huse WD, Wu H;
 XX
 DR WPI; 2001-050110/06.
 XX
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis.
 XX
 PS Disclosure; Fig 1; 132pp; English.
 CC The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta₃ integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta₃-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 XX osteoporosis.
 SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 86.1%; Score 302.2; DB 22; Length 351;
 Best Local Similarity 91.9%; Pred. No. 1.5e-80;
 Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AAGTCAGCTGTGGAGTCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTGAGACTCT 61
 Db 2 agtgcagctgtgtgagctggggagggcgtgtgtgcagcctggagggctccctgagactct 61
 QY 62 CTTGTCAGCTCTGATTCGGTCTTTCAGTAGCTATGACATGTCTGGGTCCGCAATTC 121
 Db 62 cctgtgcagcctctgattcaccttcagtagctatgacatgtctgggtccgaggtc 121
 QY 122 CGGAGAGAGGCTGGAGTGGGTGCGGAAAGTTAGTAGTGGTGGTGTAGCCTACTATT 181

Db 122 cgggcaaggctgtgagtggtgcgaaaagttagtagtggtgtagcactactatt 181
 QY 182 TAGACACTGTGTCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGACACCCATATACC 241
 Db 182 tagacactgtgcagggccgattccaccatctccagagacaatagtagaagacacccataacc 241
 QY 242 TGCAGTACGAGCTGTAAGTCTGAGGACACAGCCAGTATTACTGTGCAAGACATAACT 301
 Db 242 TGCAGTACGAGCTGTAAGTCTGAGGACACAGCCAGTATTACTGTGCAAGACATAACT 301
 QY 302 ACGGAGTATTTGCTTACTGGGCCAAGGAGGACTGTGTCATCTCTCTCT 348
 Db 302 ACGGAGTATTTGCTTACTGGGCCAAGGAGGACTGTGTCATCTCTCTCT 348

RESULT 6
 AAQ68650
 ID AAQ68650 standard: DNA; 413 BP.
 XX
 AC AAQ68650;
 XX
 DT 13-FEB-1995 (first entry)
 XX
 DE MAb A33 heavy chain coding sequence.
 XX
 KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;
 KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;
 KW secretion; A33; Fab'(gamma4deltaCys); PGL6; ompa signal; C-kappa;
 KW PSKMPA; PMR055; CH1 domains; hinge; deltaCys; PMR022; PRL09;
 KW antigen; diagnosis; treatment; colorectal cancer; metastases; ss.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT primer_bind 1..32 /*tag= a
 FT CDS 6..413 /*tag= b
 FT sig_peptide 6..62 /*tag= c
 FT mat_peptide 63..413 /*tag= d
 FT primer_bind 396..413 /*tag= e
 XX
 PN WO9413805-A.
 XX
 PD 23-JUN-1994.
 XX
 PF 10-DEC-1993; 93WO-GB02529.
 XX
 PR 10-DEC-1992; 92GB-0025853.
 PR 22-JUL-1993; 93GB-0015249.
 XX
 PA (CLIT) CELLTECH LTD.
 XX
 PI Adair JR, King DJ, Owens RJ;
 XX
 DR WPI; 1994-217881/26.
 DR P-PSDB; AAR56962.
 XX
 PT Humanised antibodies raised against A33 antigen - are used for
 PT diagnosis or treatment of colorectal tumours and metastases
 XX
 PS Example 1; Fig 3(ii); 90pp; English.
 CC The sequences given in AAQ68649-50 encode the light and heavy chain
 CC variable regions (VH and VL) of the humanised anti-A33 antibody of
 CC the invention. These fragments were produced by PCR using the primer
 CC sequences given in AAQ68624-48. The amplified fragments were used in
 CC the construction of vectors for the expression and secretion of the

CC chimeric humanised A33. The amplified products were cleaved with BstBI
 CC and SphI for the light chain and HindIII and ApaI for the heavy chain.
 CC These fragments were cloned into the human kappa light chain acceptor
 CC vector, pMR15.1, and the human heavy chain, IgG1, acceptor vector,
 CC pMR101, respectively, to give chimeric expression vector pRO108 for the
 CC light chain and pRO107 for the heavy chain. Proteins which bind the A33
 CC antigen can be used in the diagnosis or treatment of colorectal cancers
 CC and metastases.
 XX
 SQ Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;

Query Match 84.5%; Score 296.6; DB 15; Length 413;
 Best Local Similarity 90.3%; Pred. No. 7.2e-79;
 Matches 317; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTGTAGTGAAGCTGGAGGTCCTGAGACTC 60
 DB 63 gaagtgaagctgtgagctgggagcttagtaggaagctggaggggtccctgaaactc 122
 QY 61 TCCTGTGACGCTGCTGATTCGCTTTTCAGTATGCTATGACATGCTTGGGTTCGCCAGATT 120
 DB 123 tctctgtcgcctctgagctgttccttcagctacatgacatgcttgggtctgcgcgact 182
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180
 DB 183 ccggagaagagctgtgagctggggtgcgaaccttagtagtggtgtgtacacctactat 242
 QY 181 TTAGACACTGTGCGAGGCGGATTCACATCTCCAGAGACAAATGCCAAGAACCCCTATAC 240
 DB 243 tttagacagtgtgaagggcgattccaccatctccagagacagtcgaggaacacctatc 302
 QY 241 CTGCAAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGATTTACTGTGCAACACATAAC 300
 DB 303 ctgcaaatgagcagctgtgagctgtgaggaacagcgcttattactgtgcacgactacg 362
 QY 301 TAGCGCAGTTTCTTACTGAGGCGCCAGGAGCTGTGGTACTGCTCTGTGCA 351
 DB 363 gtagtcccgcttcttactgagggccaggaagctgtggtcaccgtctctgtca 413

RESULT 7
 AAV99765
 ID AAV99765 standard; DNA; 721 BP.
 AC AAV99765;
 XX
 DT 23-MAR-1999 (first entry)
 XX
 DE A33/212 single-chain Fv coding sequence.
 XX
 KW Linker: fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
 KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;
 KW aggregation; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..711
 FT /*tag= a
 FT /product= "A33/212 scFv"
 FT /note= "the start codon is not indicated"
 FT misc_feature 1..321
 FT /*tag= b
 FT /note= "sequence coding for A33 V1 region"
 FT misc_feature 322..363
 FT /*tag= c
 FT /note= "sequence coding for peptide linker 212"
 FT misc_feature 364..708
 FT /*tag= d
 FT /note= "sequence coding for A33 Vh region"
 XX
 US5856456-A.

XX
 PD 05-JAN-1999.
 XX
 PF 07-APR-1994; 94US-0224591.
 XX
 PR 07-APR-1994; 94US-0224591.
 PR 20-NOV-1992; 92US-0980529.
 PR 15-JAN-1993; 93US-0002845.
 XX
 PA (ENZO-) ENZON INC.
 XX
 PI Filpula DR, Whitlow MD;
 XX
 WPI: 1999-105193/09.
 DR
 DR P-PSDB; AAW95440.
 XX
 XX DNA encoding fusion polypeptide including protease resistant linker
 PT - for making single-chain Fv antibody fragments, e.g for diagnosis
 PT and treatment of cancer
 XX
 PS Disclosure; Fig 12; 39pp; English.
 XX
 CC The invention is directed to a novel peptide linker useful for connecting
 CC polypeptide constituents into a novel linked fusion polypeptide. The
 CC peptide linker includes at least one XP motif (where X is a charged
 CC amino acid) and includes any of these sequences (GTSXSGXPSGSGEGSTKG;
 CC GTSXSGXPSGSGSTKG; or GTSXSGXSGKG) to inhibit its proteolysis by
 CC subtilisin or trypsin. DNA molecules encoding fusion polypeptides
 CC containing two polypeptides, derived from the same multichain protein of
 CC the immunoglobulin (Ig) superfamily and a peptide linker as above, are
 CC particularly useful to prepare single chain antibody Fv fragments (scFv),
 CC potentially useful for diagnosis and treatment of cancer. The fusion
 CC polypeptide containing the specified linkers is proteolytically stable
 CC (associated with positioning of the P residue) and resistant to
 CC aggregation, while residue X improves solubility. The present sequence
 CC represents the nucleotide sequence of a A33/212 scFv fragment.
 XX
 SQ Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

Query Match 83.6%; Score 293.6; DB 20; Length 721;
 Best Local Similarity 90.2%; Pred. No. 6.6e-78;
 Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTGTAGTGAAGCTGGAGGTCCTGAGACTC 60
 DB 364 gaagtgaagctgtgagctgggagcttagtaggaagctggaggggtccctgaaactc 423
 QY 61 TCCTGTGACGCTCTGATTCGCTTTTCAGTATGCTATGACATGCTTGGGTTCGCCAGATT 120
 DB 424 tctctgtcgcctctgagctgttccttcagctacatgacatgcttgggttcgagact 483
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180
 DB 484 ccggagaagagctgtgagctggggtcgcaaccttagtagtggtgtgtacacctactat 543
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAAATGCCAAGAACCCCTATAC 240
 DB 544 tttagacagtgtgaagggcgattccaccatctccagagacagtcgaggaacacctatc 603
 QY 241 CTGCAAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGATTTACTGTGTGAAGACATAAC 300
 DB 604 ctgcaaatgagcagctgtgagctgggaggaacagcgcttattactgtgcacgactacg 663
 QY 301 TAGCGGAGTTTCTTACTGAGGCGCCAGGAGCTGTGGTACTGCTCTCT 348
 DB 664 gtagtcccgcttcttactgagggccaggaagctgtggtcactgtctct 711
 RESULT 8
 AAV99765
 ID AAV99765 standard; DNA; 721 BP.
 XX

```
AC AA237397;
XX
XX 08-FEB-2000 (first entry)
XX
XX Linked fusion protein A33/212 sfv coding sequence.
XX
XX Fusion protein; linker; linked fusion polypeptide; multichain protein;
KW protein complex; antibody; ss.
XX
XX Synthetic.
XX
XX US990275-A.
PN
XX
XX 23-NOV-1999.
XX
XX 10-SEP-1997; 97US-0926789.
XX
XX 07-APR-1994; 94US-0224591.
PR
XX 20-NOV-1992; 92US-0980529.
PR
XX 15-JAN-1993; 93US-0002845.
XX
XX (ENZO-) ENZON INC.
XX
XX Filpula DR, Whitlow MD;
PI
XX WPI; 2000-022812/02.
XX
XX Peptide linkers, linked fusion polypeptides containing the linkers and
PT their preparation -
XX
XX Example; Fig 12; 42pp; English.
XX
XX This sequence encodes a linked fusion protein containing the
CC amino acid linker of the invention. The linkers are used for connecting
CC constituent polypeptides to form novel linked fusion polypeptides.
CC Polypeptides derived from any protein can be connected, in particular
CC multichain protein or protein complexes e.g. enzymes, members of the
CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
CC provides fusion proteins which have greater stability and are less
CC susceptible to aggregation.
XX
XX Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

Query Match      83.6%; Score 293.6; DB 21; Length 721;
Best Local Similarity 90.2%; Pred. No. 6.6e-78;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTGAGACTC 60
Db 364 gaagtgaagcttggagctggggaggcttagtgaagccctggagggtccctgaaactc 423

QY 61 TCCTGTGCAGCCTCGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTGCGCAGATT 120
Db 424 tccgtgcagccctcggatcttcagtagcctatgacatgcttgggttcgcagact 483

QY 121 CCGGAGACAGAGCTGGAGTGGGTGCGAAAGTTAGTGGTGGTAGCAGCTACTAT 180
Db 484 ccgagagagagctgagtggtgctgaaccattagtagtggttagttacactactat 543

QY 181 TTAGACACTGTGCAGGGCCGATTCACATCTCCAGAGACAAATGCCAAGAACACCTATAC 240
Db 544 ttgacagtgtagagggccgattccaccatctccagagacagtgccaggaacacccctatc 603

QY 241 CNGCAANTGACAGCTGACACTGACAGACACAGCCAGTATTACTGTGCAAGACATAAC 300
Db 604 cngcaaatgacagctgacactgacagacacagccagtgatttactgtgacccgactacg 663

QY 301 TACGCACTTTTGGCTTACTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 348
Db 664 gtgctccgcttctgcttactggggcccaaggagactctggtcactgtctct 711
```

```
RESULT 9
AAV99766
ID AAV99766 standard; DNA; 733 BP.
XX
XX AAV99766;
AC
XX 23-MAR-1999 (first entry)
DT
XX A33/218 single-chain Fv coding sequence.
DE
XX Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;
KW aggregation; ds.
XX
XX Synthetic.
OS
XX
XX Location/Qualifiers
FH Key
FT CDS
FT 1..711
FT /tag= a
FT /product= "A33/218 scFv"
FT /note= "the start codon is not indicated"
FT 1..321
FT /tag= b
FT /note= "sequence coding for A33 V1 region"
FT 322..375
FT /tag= c
FT /note= "sequence coding for peptide linker 218"
FT 376..708
FT /tag= d
FT /note= "sequence coding for A33 Vh region"
FT
XX
XX US5856456-A.
PN
XX
XX 05-JAN-1999.
PD
XX 07-APR-1994; 94US-0224591.
PF
XX 07-APR-1994; 94US-0224591.
PR
XX 20-NOV-1992; 92US-0980529.
PR
XX 15-JAN-1993; 93US-0002845.
XX
XX (ENZO-) ENZON INC.
XX
XX Filpula DR, Whitlow MD;
PI
XX WPI; 1999-105193/09.
DR
XX P-PSDB; AAW93441.
XX
XX DNA encoding fusion polypeptide including protease resistant linker
PT - for making single-chain Fv antibody fragments, e.g for diagnosis
PT and treatment of cancer
XX
XX Disclosure; Fig 13; 39pp; English.
XX
XX The invention is directed to a novel peptide linker useful for connecting
CC polypeptide constituents into a novel linked fusion polypeptide. The
CC peptide linker includes at least one XP motif (where x is a charged
CC amino acid) and includes any of these sequences (GTSGSGXPGSGSGSTKG;
CC GTSGSGXPGSGSTKG; or GTSGSGSEKKG) to inhibit its proteolysis by
CC subtilisin or trypsin. DNA molecules encoding fusion polypeptides
CC containing two polypeptides, derived from the same multichain protein of
CC the immunoglobulin (Ig) superfamily and a peptide linker as above, are
CC particularly used to prepare single chain antibody Fv fragments (scFv),
CC potentially useful for diagnosis and treatment of cancer. The fusion
CC polypeptide containing the specified linkers is proteolytically stable
CC (associated with positioning of the P residue) and resistant to
CC aggregation, while residue X improves solubility. The present sequence
CC represents the nucleotide sequence of a A33/218 scFv fragment.
XX
XX Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;
SQ
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Query Match 83.6%; Score 293.6; DB 20; Length 733;

Best Local Similarity 90.2%; Pred. No. 6.6e-78;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCGAGCTGGAGCTCTGGGGAGGCTTAGTGAAGCCTGGAGCTCCCTGAGACTC 60
Db 376 gaagtgaagcctgtggaagctctgggagggcttagtgaagcctggaggtccctgaaactc 435
QY 61 TCCGTGTCAGCCTCTGGATTGCGTTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGATT 120
Db 436 tccgtgcagcctctggattcgcttccagttacattgacatgtcttgggttcgcagact 495
QY 121 CCGAGAGAGCGCTGGAGTGGTGCCTTCAAGATTAGTAGTGTGGTGGTAGCACTACTAT 180
Db 496 ccgagagaagagcctggagtggtgcgaaccatttagtggtgtagttacacactactat 555
QY 181 TTAGACACTGTGTCAGGCGCGATTCCACCATCTCCAGAGACAAATGCCAAGAACACCTATAC 240
Db 556 ttagacagtgtgaagggccgattccaccattccagagacagtgccaggaacacccctatac 615
QY 241 CTGCAATGAGCACTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 616 ctgcaaatgagcagctcgaggtctgagacacgacctgtattactgtgcaccgactacg 675
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGGACTCTGGTCACTGTCTCT 348
Db 676 gtatgccgtttgtctactggtgccaagggactctgtgtcactgtctct 723

RESULT 10
AAZ37398
ID AAZ37398 standard; DNA; 733 BP.
XX
AC AAZ37398;
XX
DT 08-FEB-2000 (first entry)
XX
DE Linked fusion protein A33/218 sFv coding sequence.
XX
KW Fusion protein; linker; linked fusion polypeptide; multichain protein;
KW protein complex; antibody; ss.
XX
OS Synthetic.
XX
PN US5990275-A.
XX
PD 20-NOV-1992; 92US-0980529.
XX
PR 15-JAN-1993; 93US-0002845.
XX
PA (ENZO-) ENZON INC.
XX
PI Filpula DR, Whitlow MD;
XX
XX WPI: 2000-022812/02.
DR P-PSDB; AAY54837.
XX
XX Peptide linkers, linked fusion polypeptides containing the linkers and
PT their preparation -
XX
XX Example; Fig 13; 42pp; English.
XX
XX This sequence encodes a linked fusion protein containing the
CC amino acid linker of the invention. The linkers are used for connecting
CC constituent polypeptides to form novel linked fusion polypeptides.
CC Polypeptides derived from any protein can be connected, in particular
CC multichain protein or protein complexes e.g. enzymes, members of the
CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
CC provides fusion proteins which have greater stability and are less
CC susceptible to aggregation.

XX
SQ Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 83.6%; Score 293.6; DB 21; Length 733;
Best Local Similarity 90.2%; Pred. No. 6.6e-78;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCGAGCTGGAGCTCTGGGGAGGCTTAGTGAAGCCTGGAGCTCCCTGAGACTC 60
Db 376 gaagtgaagcctgtggaagctctgggagggcttagtgaagcctggaggtccctgaaactc 435
QY 61 TCCGTGTCAGCCTCTGGATTGCGTTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGATT 120
Db 436 tccgtgcagcctctggattcgcttccagttacattgacatgtcttgggttcgcagact 495
QY 121 CCGAGAGAGCGCTGGAGTGGTGCCTTCAAGATTAGTAGTGTGGTGGTAGCACTACTAT 180
Db 496 ccgagagaagagcctggagtggtgcgaaccatttagtggtgtagttacacactactat 555
QY 181 TTAGACACTGTGTCAGGCGCGATTCCACCATCTCCAGAGACAAATGCCAAGAACACCTATAC 240
Db 556 ttagacagtgtgaagggccgattccaccattccagagacagtgccaggaacacccctatac 615
QY 241 CTGCAATGAGCACTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 616 ctgcaaatgagcagctcgaggtctgagacacgacctgtattactgtgcaccgactacg 675
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGGACTCTGGTCACTGTCTCT 348
Db 676 gtatgccgtttgtctactggtgccaagggactctgtgtcactgtctct 723

RESULT 11
AAV07642
ID AAV07642 standard; DNA; 369 BP.
XX
AC AAV07642;
XX
DT 10-DEC-1998 (first entry)
XX
DE anti-CD22 monoclonal antibody heavy chain variable region DNA sequence.
XX
KW anti-CD22 monoclonal antibody heavy chain variable region; VL;
KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
KW malignant B-cell; immunodiagnosis; RFB4 IgG; ss.
XX
OS Mammalia.
XX
XX Key Location/Qualifiers
FT CDS 1..369
FT /tag= a
FT /transl_except= (pos:361..363, aa:Thr)
FT /note= "CDS does not contain a stop codon"
XX
XX WO9841641-A1.
XX
XX 24-SEP-1998.
XX
XX 19-MAR-1998; 98WO-US05453.
XX
XX 20-MAR-1997; 97US-0041437.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
XX
XX WPI: 1998-521227/44.
DR P-PSDB; AAW66099.
XX
XX Recombinant anti-CD22 antibodies and immuno-conjugates - of
PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
PT or a label; for inhibiting malignant B-cells

CC variable domains. The amplified cDNAs were sequenced (AA062788 and
 CC AA062789). Chimeric mouse-human antibodies were constructed
 CC using human constant regions so as to produce less immunogenic
 CC polypeptides which retained the anti-human carcinoma binding
 CC specificity of KC-4.
 XX
 SQ Sequence 418 BP; 88 A; 94 C; 136 G; 110 T; 0 other;

Query Match 80.9%; Score 284; DB 15; Length 418;
 Best Local Similarity 89.2%; Pred. No. 4e-75;
 Matches 321; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

QY 1 GAAGTCAGCTGGTGGAGCTGGGGAGCTTAGTGAAGCTGGAAGTCCCTGAGACTC 60
 DB 58 gaagtacagatggtgagctctggggagagcttagtgaagcctggaggtccctgaaactc 117
 QY 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTTGGGTTGCCAGATT 120
 DB 118 tctgtgcagcctctgattcgctttcagtagctatgccatgtcttgggttcgagctct 177
 QY 121 CCGGAGAAGAGCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
 DB 178 ccagagaagagcctgagtggtgctgcagaaatagtagtgggttaattacccttactat 237
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
 DB 238 caagacactgtgacggcgcttaccatctccagagacaatgccaaagacaccctgtac 297
 QY 241 CTGCAATGAGCACTGTAAGTCTGAGGACACAGCCATGTTACTGTGCAAGACATAAC 300
 DB 298 ctggaatagcagctgagtggtgctgagcacagcgccatgtattactgtcaaggaggac 357
 QY 301 TACGG-----CAGTTTGTCTACTGGGCCAAGGACTGTGCTACTGTCTCTGCA 351
 DB 358 tacggtatcccgccctggttcttactggggccaaaggactctggtctctctctgca 417

RESULT 15
 AAV24232
 ID AAV24232 standard; cDNA to mRNA; 411 BP.
 XX
 AC AAV24232;
 XX
 DT 03-SEP-1998 (first entry)
 XX
 DE Chimeric antibody against hTPR H chain V region cDNA SEQ ID NO:57.
 KW Chimeric; antibody; human parathormone related peptide; hTPR; mouse;
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised; ds.
 XX
 OS Synthetic.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..411
 FT /tag= a
 FT /note= "no stop codon given"
 FT sig_peptide 1..57
 FT /tag= b
 FT mat_peptide 58..411
 FT /tag= c
 XX
 PN WO9813388-A1.
 XX
 PD 02-APR-1998.
 XX
 PF 24-SEP-1997; 97WO-JP03382.
 XX
 PR 24-JUL-1997; 97JP-0214168.

PR 26-SEP-1996; 96JP-0255196.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Sato K, Wakahara Y, Yabuta N;
 PI WPI; 1998-230640/20.
 DR P-PSDB; AA57592.
 XX
 PT New chimeric antibodies against human parathormone related
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 PT disorders caused by malignant neoplasm(s)
 XX
 PS Claim 52; Page 120-121; 182pp; Japanese.
 XX
 CC New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPRP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence encodes a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphemia such as that due to
 CC pathogens or to vitamin D resistance.
 XX
 SQ Sequence 411 BP; 98 A; 97 C; 109 G; 107 T; 0 other;

Query Match 80.8%; Score 283.6; DB 19; Length 411;
 Best Local Similarity 89.5%; Pred. No. 5.2e-75;
 Matches 317; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 1 GAAGTCAGCTGGTGGAGCTGGGGAGGCTTAGTGAAGCTGGAAGTCCCTGAGACTC 60
 DB 58 gaggtgcaactggtgagctgctggggagagacttagtgaagcctggaggggtccctgaaactc 117
 QY 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTTGGGTTGCCAGATT 120
 DB 118 tctgtgcagcctctggttccacttccagtagctatgcatgtcttggattcgagact 177
 QY 121 CCGGAGAAGAGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
 DB 178 ccagacaagagctgagtggtgctgcgaaccattagtagtgggttagttacacctactat 237
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
 DB 238 ccagacagctgtgaaagggtgctccaccatctccagagacaatgccaaagacacccctatc 297
 QY 241 CTGCAATGAGCAGCTCTGAACCTCTGAGGACACAGCCATGTTACTGTGCAAGACATAAC 300
 DB 298 ctgcaaatgagcagctgaaagtctgagcacagccatgttttactgtgcaagagact 357
 QY 301 TACGGCAGT---TTTGGCTTACTGGGGCCCAAGGACTCTGGTCTACTGTCTCTGCA 351
 DB 358 actatgacttacttcttactggtgggcaaggagactgtgctcactgtctctgca 411

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
755.608 Million cell updates/sec

Title: US-08-791-391A-5

Perfect score: 351

Sequence: 1 GAAGTGCAGCTGGTGGAGTC.....CTCTGGTCACTGTCTCTGCA 351

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Post-processing: Minimum Match 0%

Maximum Match 100%

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 - 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
 - 5: /cgn2_6/ptodata/2/ina/PCRUS_COMB.seq.*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	84.0	413	1	US-08-253-877C-56
2	295	84.0	413	2	US-08-452-164A-56
3	293.6	83.6	721	2	US-08-224-591-15
4	293.6	83.6	721	2	US-08-926-789-15
5	293.6	83.6	733	2	US-08-224-591-17
6	293.6	83.6	733	2	US-08-926-789-17
7	284	80.9	418	1	US-07-977-696C-27
8	284	80.9	418	1	US-08-129-930B-27
9	279	79.5	354	4	US-08-487-761-14
10	271	77.2	445	1	US-08-053-171-10
11	271	77.2	491	1	US-08-053-171-6
12	269.4	76.8	923	5	PCT-US94-07659-1
13	267.8	76.3	357	2	US-08-475-000-15
14	267.8	76.3	357	2	US-08-483-199-15
15	267.8	76.3	357	2	US-08-484-508-15
16	266.2	75.8	357	1	US-08-331-398A-21
17	266.2	75.8	357	1	US-08-859-649-26
18	266.2	75.8	357	2	US-08-331-397B-21
19	266.2	75.8	357	2	US-08-759-804A-21
20	266.2	75.8	375	1	US-08-331-398A-59
21	266.2	75.8	375	2	US-08-331-397B-59
22	266.2	75.8	375	2	US-08-759-804A-58
23	264.6	75.4	357	1	US-08-385-936-1
24	264.6	75.4	357	1	US-08-487-860-1
25	263	74.9	357	1	US-08-285-936-5
26	263	74.9	357	1	US-08-487-860-5

28	263	74.9	357	1	US-08-487-860-7	Sequence 7, Appl
29	263	74.9	357	2	US-08-553-497A-17	Sequence 17, Appl
30	262.2	74.7	357	1	US-08-207-996-26	Sequence 26, Appl
31	262.2	74.7	357	2	US-08-760-840A-26	Sequence 26, Appl
32	262.2	74.7	357	3	US-08-760-840A-27	Sequence 27, Appl
33	262.2	74.7	357	3	US-09-266-119-26	Sequence 26, Appl
34	262.2	74.7	357	3	US-09-266-119-27	Sequence 27, Appl
35	262	74.6	357	2	US-07-956-399-3	Sequence 3, Appl
36	261.4	74.5	357	1	US-08-285-936-11	Sequence 11, Appl
37	261.4	74.5	357	1	US-08-487-860-11	Sequence 11, Appl
38	259.8	74.0	357	1	US-08-487-860-56	Sequence 56, Appl
39	259.8	74.0	405	4	US-08-579-378A-15	Sequence 15, Appl
40	259.6	74.0	417	1	US-08-398-613A-21	Sequence 21, Appl
41	259.6	74.0	417	1	US-08-398-612A-21	Sequence 21, Appl
42	259.6	74.0	417	1	US-08-398-611A-21	Sequence 21, Appl
43	259.6	74.0	417	1	US-08-396-851A-21	Sequence 21, Appl
44	259.6	74.0	417	2	US-08-491-334A-21	Sequence 21, Appl
45	259.6	74.0	417	3	US-09-027-449-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-253-877C-56
; Sequence 56, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Himman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Kwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
US-08-253-877C-56

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
; US-08-452-164A-56

Query Match      84.08; Score 295; DB 2: Length 413;
Best Local Similarity 90.08; Pred. No. 9.7e-85;
Matches 316; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      1  GAAGTGCAGCTGTGTGGAGTCTGTGGGGGAGGCTTACTGAAGCCTGGAAGTCTCCTCGAGACTC 60
      |||||
Db      63  GAAGTGAAGCTGTGTGGAGTCTGTGGGGAGGCTTACTGAAGCCTGGAGGCTCCTGAAACTC 122

QY      61  TCCTGTGCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGATT 120
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Db     123  TCCTGTGCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGACT 182

QY     121  CCGGAGAAGAGGCTGTGGAGTGGGTCCGAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
      |||||
Db     183  CCGGAGAAGAGGCTGTGGAGTGGGTCCGAACCATTAGTAGTGGTGGTAGTACACCTACTAT 242

QY     181  TTAGACACTGTGCAGGGCCGATTCACCATCTCCAGAGACAATGCCAGACACACCCCTATAC 240
      |||||
Db     243  TTAGACAGTGTGAAGGGCCGATTCCACATCTCCAGAGACAGTCCCGAGGAACACCCCTATAC 302

QY     241  CTGCAAAATGAGCAGTCTGAACTCTGAGGACACAGCCATGTTACTGTGCAAGACATAAC 300
      |||||
Db     303  CTGCAAAATGAGCAGTCTGAGGCTGTGAGGACACGGCCCTGTATTACTGTGCACCGACTACG 362

QY     301  TACGGCAGTTTTGCTTACTGGGGCCAAAGGACTCTGCTACTGTCTCTGCA 351
      |||||
Db     363  GTAGTCCCGTTTGTCTTACTGGGGCCAAAGGACTCTGCTCACCGTCTCTGCA 413
      |||||

```

RESULT 3
US-08-224-591-15
; Sequence 15, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-224-591-15

Query Match 83.6%; Score 293.6; DB 2; Length 721;
Best Local Similarity 90.2%; Pred. No. 3.3e-84;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GAAGTGACGCTGGAGCTGCGGAGGCTTAGTGAAGCCTGGAAGCTCCCTGAGACTC 60
Db 364 GAAGTGAAGCTTGTGGAGCTGCGGAGGCTTAGTGAAGCCTGGAAGCTCCCTGAAACTC 423
Qy 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120
Db 424 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGACT 483
Qy 121 CCGGAGAAGAGCGCTGGAGTGGGTCGCAAAAGCTTAGTGTGCTGGTGGTAGCACCTACTAT 180
Db 484 CCGGAGAAGAGCGCTGGAGTGGGTCGCAAAAGCTTAGTGTGCTGGTGGTAGCACCTACTAT 543
Qy 181 TTAGACACTGTGCGAGGCGCGATTACCATCTCCAGAGACAAATGATGTCGAGCAACCTATAC 240
Db 544 TTAGACACTGTGCGAGGCGCGATTACCATCTCCAGAGACAAATGATGTCGAGCAACCTATAC 603
Qy 241 CTGCAATGACAGCTGCAACTCTGAGGACACGCCATGATGTCGTCAGCAAGACTAC 300
Db 604 CTGCAATGACAGCTGCAACTCTGAGGACACGCCATGATGTCGTCAGCAAGACTAC 663
Qy 301 TACGGCAGTTTGTCTTACTTGGGGCCAGGAGCTCTGGTCACTGTCTCT 348
Db 664 GTAGTCCCGTTTGTCTTACTTGGGGCCAGGAGCTCTGGTCACTGTCTCT 711

RESULT 4
US-08-926-789-15
; Sequence 15, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-926-789-15

Query Match 83.6%; Score 293.6; DB 2; Length 721;
Best Local Similarity 90.2%; Pred. No. 3.3e-84;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GAAGTGACGCTGGAGCTGCGGAGGCTTAGTGAAGCCTGGAAGCTCCCTGAGACTC 60
Db 364 GAAGTGAAGCTTGTGGAGCTGCGGAGGCTTAGTGAAGCCTGGAAGCTCCCTGAAACTC 423
Qy 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120
Db 424 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGACT 483
Qy 121 CCGGAGAAGAGCGCTGGAGTGGGTCGCAAAAGCTTAGTGTGCTGGTGGTAGCACCTACTAT 180
Db 484 CCGGAGAAGAGCGCTGGAGTGGGTCGCAAAAGCTTAGTGTGCTGGTGGTAGCACCTACTAT 543
Qy 181 TTAGACACTGTGCGAGGCGCGATTACCATCTCCAGAGACAAATGATGTCGAGCAACCTATAC 240
Db 544 TTAGACACTGTGCGAGGCGCGATTACCATCTCCAGAGACAAATGATGTCGAGCAACCTATAC 603
Qy 241 CTGCAATGACAGCTGCAACTCTGAGGACACGCCATGATGTCGTCAGCAAGACTAC 300
Db 604 CTGCAATGACAGCTGCAACTCTGAGGACACGCCATGATGTCGTCAGCAAGACTAC 663
Qy 301 TACGGCAGTTTGTCTTACTTGGGGCCAGGAGCTCTGGTCACTGTCTCT 348
Db 664 GTAGTCCCGTTTGTCTTACTTGGGGCCAGGAGCTCTGGTCACTGTCTCT 711

RESULT 5
US-08-224-591-17
; Sequence 17, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591

Patent No. 6217866
 GENERAL INFORMATION:
 APPLICANT: Schlusser, Joseph
 APPLICANT: Givol, David
 APPLICANT: Bellot, Françoise
 APPLICANT: Kris, Richard
 APPLICANT: Ricca, George A.
 APPLICANT: Cheadle, Christopher
 APPLICANT: South, Victoria J.
 TITLE OF INVENTION: Monoclonal Antibodies Specific to Human
 TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods
 NUMBER OF INVENTIONS: 17
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.0 (Patentin)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,761
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/086,411
 FILING DATE: 29-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Goodman, Rosanne
 REGISTRATION NUMBER: 32,534
 REFERENCE/DOCKET NUMBER: A0207C-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 454-3817
 TELEFAX: (215) 454-3808
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 354 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..354
 US-08-487-761-14

Query Match 79.5%; Score 279; DB 4; Length 354;
 Best Local Similarity 90.5%; Pred. No. 1,1e-79;
 Matches 323; Conservative 0; Mismatches 25; Indels 9; Gaps 2;
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 Db 1 GAAGTCACGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAAGGTCCTGGAAGT 60
 QY 61 TCCTGTGACGCTCTGGATTCGCTTTCAGTAGTATGATGATGCTTGGGTTGCCGAGATT 120
 Db 61 TCCTGTGACGCTCTGGATTCGCTTTCAGTAGTATGATGATGCTTGGGTTGCCGAGACT 120
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAAAGTATAGTAGTGGTGGTGGTGGTGGTGGTGGT 180
 Db 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAAAGTATAGTAGTGGTGGTGGTGGTGGTGGTGGT 177
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
 Db 178 CCAGACACTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 237
 QY 241 CTGCAANTAGCAGCTGAACTCTGAGGACACAGCCATGATGATGTCGCAAGACA ---- 296

Db 238 CITCAAAATGAGCAGTCTGAAGTCTGAGGACACAGCCATTATTACTGTGCAAGTCACTAT 297
 QY 297 --TAAGTACGGCAGTTTCTGCTTACTGGGGCCCAAGGACTCTGGTCACTGTCTGTGCA 351
 Db 298 GGTACGACGGGAGGTTGCTTACTGGGGCCCAAGGACTCTGGTCACTGTCTGTGCA 354
 RESULT 10
 US-08-053-171-10
 ; Sequence 10, Application US/08053171
 ; Patent No. 5562903
 ; GENERAL INFORMATION:
 ; APPLICANT: Co, Loibner
 ; TITLE OF INVENTION: Antibody Derivatives
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Hourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/053,171
 ; FILING DATE: 22-APR-1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-54-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1..445
 ; OTHER INFORMATION: /standard_name= "Heavy Chain
 ; OTHER INFORMATION: V-region of BR55-2 Antibody in pVg-1c and pVg-3c"
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 12..425
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1..6
 ; OTHER INFORMATION: /standard_name= "Xba I restriction
 ; OTHER INFORMATION: site"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 440..445
 ; OTHER INFORMATION: /standard_name= "Xba I restriction
 ; OTHER INFORMATION: site"
 ; US-08-053-171-10

Query Match 77.2%; Score 271; DB 1; Length 445;
 Best Local Similarity 87.1%; Pred. No. 4.2e-77;
 Matches 311; Conservative 0; Mismatches 40; Indels 6; Gaps 1;
 QY 1 GAAGTCACGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAAGGTCCTGAGACTC 60

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 169..909
PCT-US94-07659-1

Query Match 76.8%; Score 269.4; DB 5; Length 923;
Best Local Similarity 86.8%; Pred. No. 1.8e-76;
Matches 310; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
QY 1 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAAGCTCCCTGAGACTC 60
DB 226 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAACTC 285
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTTCAGTAGCTATGACATGCTCTTGGGTTGCCAGATT 120
DB 286 TCCTGTGAGCCTCTGGATTCGCTTTTTCAGTAGCTATGACATGCTCTTGGGTTGCCAGACT 345
QY 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGACCTACTAT 180
DB 346 CCGGAGAAGAGCTGGAGTGGGTCGCAATACATTAGTAGTGGTGGTAGGACCTACTAT 405
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
DB 406 CCAGACACTGTGAAGGCGGATTCACCATCTCCAGGACAATGCCAAGAACACCCCTGTAC 465
QY 241 CTGCAATAGCAGCTGAACTCTGAGGACAGCCATGTTATCTGTGCAAGA----- 294
DB 466 CTGCAATAGCAGCTGAACTCTGAGGACAGCCATGTTATCTGTGCAAGAGGGGG 525
QY 295 CATAACTACGGCAGTTTCTTACTGGGCGCAAGGAGCTCTGTCTACTCTCTGCA 351
DB 526 GTACGAGGAGGTACTTCATGCTCTGGGCGCAGGAGGACCGTACCCTCTCTCA 582

RESULT 13
US-08-475-000-15
Sequence 15, Application US/08475000
Patent No. 5811267
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,000
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
US-08-475-000-15

Query Match 76.3%; Score 267.8; DB 1; Length 357;
Best Local Similarity 86.6%; Pred. No. 4e-76;
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;
QY 1 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAAGTCCCTGAGACTC 60
DB 1 GAGGTGAAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAACTC 60
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTTCAGTAGCTATGACATGCTCTTGGGTTGCCAGATT 120
DB 61 TCCTGTGAGCCTCTGGATTCGCTTTTTCAGTAGCTATGACATGCTCTTGGGTTGCCAGACT 120
QY 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGACCTACTAT 180
DB 121 CCGGAGAAGAGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGGTAGGACCTACTAT 180
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
DB 181 CCAGACACTGTGAAGGCTGATTCACCGTCTCCAGAGACAATGCCATGAGAGCTGTAC 240
QY 241 CTGCAATAGCAGCTGAACTCTGAGGACAGCCATGTTATCTGTGCAAGA----- 296
DB 241 CTGCAATAGCAGCTGAGGCTGAGGACAGCCCTTGTATTACTGTGCAAGATACGGG 300
QY 297 --TAAGTACGGCAGTTTCTTACTGGGCGCAAGGAGCTCTGTCTACTCTCTGCA 351
DB 301 GCTGTGAGCCTGGTTCCTTACTGGGCGCAAGGAGCTCTGTGTCACAGTTCTTCTCA 357

RESULT 14
US-08-483-199-15
Sequence 15, Application US/08483199
Patent No. 5849877
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.199
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
US-08-483-199-15

Query Match 76.3%; Score 267.8; DB 2; Length 357;
Best Local Similarity 86.6%; Pred. No. 4e-76;
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

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RESULT 15
US-08-484-508-15
Sequence 15, Application US/08484508
Patent No. 5948647
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.508
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0850.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
US-08-484-508-15

Query Match 76.3%; Score 267.8; DB 2; Length 357;
Best Local Similarity 86.6%; Pred. No. 4e-76;
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

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Search completed: October 11, 2001, 15:14:14
Job time: 5001 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:32 ; Search time 2122.65 Seconds
(without alignments)
2339.127 Million cell updates/sec

Title: US-08-791-391A-7
Perfect score: 321
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	296	92.2	321	94	AF163757 Mus muscu
4	296	92.2	321	94	M95945 Mouse mRNA
5	296	92.2	370	94	M93959 Mouse Ig ac
6	296	92.2	381	10	E07933 cDNA encodi
7	296	92.2	381	10	I31959 Sequence 82
8	296	92.2	381	10	I78571 Sequence 82


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RESULT 3
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DEFINITION mRNA, partial cds.
ACCESSION AF163757
VERSION AF163757.1 GI:5690320
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 321)
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE (bases 1 to 321)
JOURNAL Merten, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
REFERENCE 2 (bases 1 to 321)
AUTHORS Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
TITLE Mouse Monoclonal Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Mertens, N.M. and Cunningham, M.W.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
JOURNAL University Health Sciences Center, 940 St. Young Blvd, Oklahoma
JOURNAL City, OK 73190, USA
FEATURES
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ORIGIN

Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
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DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95945
VERSION M95945.1 GI:309177
KEYWORDS Mus musculus (strain BALB/c, sub_species domesticus) CDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 321)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
Co, M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
JOURNAL Untitled
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Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

CDS
1 GATATTGCTGAACCTCCTCCAGCCACCTGTGTGTGACACAGGAGATAGCGTCACT 60
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LOCUS Mouse Ig active kappa-chain V-region, partial cds.
DEFINITION M93959
ACCESSION M93959
VERSION M93959.1 GI:197572
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 370)
REFERENCE Takeda, Y., Wise, K.S. and Hoffman, R.W.
AUTHORS Nucleotide sequences of immunoglobulin heavy and light chain
TITLE V-regions from a monoclonal autoantibody specific for a unique set
of small nuclear ribonucleoprotein complexes
JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)
MEDLINE 92375706
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Best Local Similarity 95.3%; Pred. No. 1.5e-90;
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RESULT 6
E07933
LOCUS E07933 381 bp RNA 29-SEP-1997
DEFINITION CDNA encoding variable region of mouse anti-FHV-1 antibody L chain.
ACCESSION E07933
VERSION E07933.1 GI:2176065
KEYWORDS JP 1994217786-A/2.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 381)
REFERENCE Kurumi, K., Maeda, H., Nishiyama, K. and Tokiyoshi, Y.
AUTHORS ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT
TITLE ENCODING THE SAME ANTIBODY
JOURNAL Patent: JP 1994217786-A 2 09-AUG-1994;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Mus sp. (mouse)
PN JP 1994217786-A/2
PD 09-AUG-1994
PF 28-NOV-1992 JP 1992341255
PI KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI
TOKIYOSHI YUKIO
PC C12P21/08,A61K39/395,C07K15/00,C12N15/13,(C12P21/08,C12R1:91);
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QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180
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QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
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QY 301 GGGACCAAGCTGGAATTA 320
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Db 361 GGGACCAAGCTGGAGCTGAA 380

RESULT 7

LOCUS I131959 381 bp DNA PAT 06-FEB-1997

DEFINITION Sequence 82 from patent US 5585089.

ACCESSION I131959

VERSION I131959.1 GI:1822750

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 381)

AUTHORS Queen, C.L. and Selick, H.E.

TITLE Humanized immunoglobulins

JOURNAL Patent: US 5585089-A 82 17-DEC-1996;

FEATURES Location/Qualifiers

source 1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

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Qy 301 GGGACCAAGCTGGAAATCAA 320

Db 361 GGGACCAAGCTGGAAATCAA 380

RESULT 8

LOCUS I78571 381 bp DNA PAT 03-APR-1998

DEFINITION Sequence 82 from patent US 5693761.

ACCESSION I78571

VERSION I78571.1 GI:3014725

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 381)

AUTHORS Queen, C.L., Schneider, W.P. and Selick, H.E.

TITLE Polynucleotides encoding improved humanized immunoglobulins

JOURNAL Patent: US 5693761-A 82 02-DEC-1997;

FEATURES Location/Qualifiers

source 1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

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Db 301 GAAGATTTTGGAAATGTTCTCTCAACAGAGTAAACAGTAACTGCTATACCTTCGGAGGG 360

Qy 301 GGGACCAAGCTGGAAATCAA 320

Db 361 GGGACCAAGCTGGAAATCAA 380

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

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Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCTCAACAGAGTGGCAGCTGGCCTCACACAGTTCGGAGGG 300

Db 361 GGGACCAAGCTGGAAATCAA 380

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Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

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Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCTCAACAGAGTGGCAGCTGGCCTCACACAGTTCGGAGGG 300

Db 361 GGGACCAAGCTGGAAATCAA 380

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Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

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Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

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Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

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Db 361 GGGACCAAGCTGGAAATCAA 380

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db 121 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGATCCCTCC 180

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Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

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Db 361 GGGACCAAGCTGGAAATCAA 380

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60

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Db 361 GGGACCAAGCTGGAATAA 380
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RESULT 10
MUSIGKCNJ
LOCUS MUSIGKCNJ 431 bp mRNA ROD 26-MAR-1994
DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone ANLIK.
ACCESSION M19913 J03832
VERSION M19913.1 GI:197033
KEYWORDS C-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Rule, G.S.
JOURNAL Unpublished (1988)
REFERENCE 2 (bases 1 to 431)
AUTHORS Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label antibodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
MEDLINE 88234486
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by G. Rule, 20-JUL-1988.
FEATURES
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/sub_species="domesticus"
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Query Match 92.2%; Score 296; DB 94; Length 431;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACGAGAGATAGCGTCAGT 60
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QY 241 GAAGATTTTGGAAATGATTTCTGTCAACAGAGTGGCAGTGGCTCACAGCTTCGGAGGG 300
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RESULT 11
MUSCMVF
LOCUS MUSCMVF 321 bp mRNA ROD 26-JUL-1993
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95943
VERSION M95943.1 GI:309175
KEYWORDS Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S., Co, M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
JOURNAL Unpublished (1992)
TITLE Untitled
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Best Local Similarity 95.0%; Pred. No. 5.2e-90;
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Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGT 60
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Db 301 GGGACCAAGCTGGAATAA 320
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RESULT 12
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LOCUS AF139849 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable

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misc_feature 148..168
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BASE COUNT 86 a 82 c 75 g 81 t
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QY 301 GGGACCAAGCTGGAATTTAA 320
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Db 301 GGGACCAAGCTGGAATTTAA 320
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RESULT 15
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LOCUS Mus musculus clone 15 immunoglobulin kappa light chain variable
DEFINITION region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139846
VERSION AF139846.1 GI:4732156
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 324)
JOURNAL Brard F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M.
MEDLINE Somatic mutation and light chain rearrangement generate
PUBMED autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
99406777
J. Exp. Med. 190 (5), 691-704 (1999)
10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard, F. and Weigert, M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
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AUTHORS Gilbert,D.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Gilbert D., Immunology, U519 INSERM, 22 bd Gambetta, 76183 ROUEN cedex, FRANCE
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BASE COUNT 84 a 83 c 74 g 80 t
ORIGIN
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Best Local Similarity 94.4%; Pred. No. 5.6e-89;
Matches 302; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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Db 301 GGGACCAAGCTGGAGCTGAA 320

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258: gb_est189:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	266	82.9	738	150	BF582153 602099743
2	255.6	79.6	949	150	BF579007 602096124
3	233.6	72.8	624	166	BE306691 601104076
4	223.8	69.7	849	150	BF583521 602101553
5	204	63.6	708	166	BE309445 601095331
6	194.4	60.6	434	115	AW406486 UI-HF-BL0
7	192	59.8	946	155	BG569760 602590367
8	190.4	59.3	519	115	AW405183 UI-HF-BL0
9	188.8	58.8	398	115	AW405309 UI-HF-BL0
10	187.2	58.3	465	115	AW404697 UI-HF-BL0
11	187.2	58.3	468	115	AW404506 UI-HF-BL0
12	185.8	57.9	385	115	AW405025 UI-HF-BL0
13	185.6	57.8	468	115	AW405643 UI-HF-BL0
14	185.6	57.8	482	32	AV733856 AV733856
15	185.6	57.8	1015	155	BG536848 602566386
16	184.6	57.5	936	145	BF164906 601778137
17	184	57.3	514	115	AW405207 UI-HF-BL0
18	181.4	56.5	548	155	EG568486 602587455
19	180.8	56.3	519	122	AW959456 EST371526
20	180.6	56.3	1061	151	BF663663 602145371
21	179.6	56.0	330	115	AW406212 UI-HF-BL0
22	179.2	55.8	448	115	AW404726 UI-HF-BL0
23	179.2	55.8	485	110	AV734882 AV734882
24	179	55.8	451	170	BF874574 IL3-ET011
25	178.4	55.6	639	32	AV734416 AV734416
26	177.6	55.3	409	115	AW406057 UI-HF-BL0
27	177.4	55.3	461	115	AW406219 UI-HF-BL0
28	176.6	55.0	868	155	BG539952 602567464
29	175.4	54.6	413	115	AW406440 UI-HF-BL0
30	175.4	54.6	489	115	AW406154 UI-HF-BL0
31	175.2	54.6	656	154	BG482934 602502942
32	174.6	54.4	576	115	AW378342 RCO-HT021
33	174.4	54.3	443	115	AW405460 UI-HF-BL0
34	174.4	54.3	748	154	BG529887 602558987
35	174.2	54.3	758	154	BG534598 602553450
36	173	53.9	317	115	AW404261 UI-HF-BL0
37	172.6	53.8	504	115	AW405787 UI-HF-BL0
38	171	53.3	369	115	AW405943 UI-HF-BL0
39	170	53.0	473	115	AW406934 UI-HF-BL0
40	169.6	52.8	425	115	AW406785 UI-HF-BL0
41	169.6	52.8	514	169	BF747264 RCL-BT025
42	169.6	52.8	604	115	AW405198 UI-HF-BL0
43	169.4	52.8	518	115	AW406576 UI-HF-BL0
44	169.4	52.8	644	115	AW405817 UI-HF-BL0
45	169.4	52.8	661	32	AV693657 AV693657

ALIGNMENTS

RESULT	1
BF582153	
LOCUS	BF582153
DEFINITION	602099743F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4219402 5', mRNA sequence.
ACCESSION	BF582153
VERSION	BF582153.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 738)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: Jeffrey E. Green, M.D.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLAM9801	row: f column: 11
High quality sequence stop: 714.	
Location/Qualifiers	
1. 738	
/organism="Mus musculus"	
/strain="FVB/N"	
/db_xref="taxon:10090"	
/clone="IMAGE:4219402"	
/clone_lib="NCI_CGAP_Co24"	
/lab_host="DH10B (T1 phage-resistant)"	
/note="organ: Colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	210 a 189 c 172 g 167 t
ORIGIN	
Query Match	82.9%; Score 266; DB 150; Length 738;
Best Local Similarity	94.0%; Pred No. 2e-74; 15; Indels 4; Gaps 2;
Matches 299; Conservative 0; Mismatches 15; Indels 4; Gaps 2;	
QY	6 TGTGTAACAGTCTCCAGCCACCTGTCGTGTGACACGAGATAGCGTCAGTCTTTC 65
DB	78 TGTGTAACAGTCTCCAGCCACCTGTCGTGTGACACGAGATAGCGTCAGTCTTTC 137
QY	66 CTGCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAATCATGA 125
DB	138 CTGCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAATCATGA 197
QY	126 GTCCTCAAGCTTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 185
DB	198 GTCCTCAAGCTTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 257
QY	186 CAGTGGCAGTGGATCAGGACAGATTTTCGTCTCAGTATCAACAGTGTGGAGACTGAAGA 245
DB	258 CAGTGGCAGTGGATCAGGACAGATTTTCGTCTCAGTATCAACAGTGTGGAGACTGAAGA 317
QY	246 TTTTGGATGATTTCTGTCAACAGAGTGGAGCTGGCCCTCA---CACGTTCCGAGGGGG 302
DB	318 -TTTGGATGATTTCTGTCAACAGAGTAAACAGTGGCTCAGCTCAGCTTCGGTCTGG 376
QY	303 GACCAAGCTGGAAATTA 320
DB	377 GACCAAGCTGGAGCTGA 394
RESULT	2
BF579007	
LOCUS	BF579007 949 bp mRNA
DEFINITION	602096124F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4216180 5', mRNA sequence.
ACCESSION	BF579007
VERSION	BF579007.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 949)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 519)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
SOURCE

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i. 0.319
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058506"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (ITI)"
/notes="Vector: pV7r3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Ronaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      127 a      153 c      126 g      112 t      1 others
ORIGIN

Query Match      59.3%;      Score 190.4;      DB 115;      Length 519;
Best Local Similarity 74.7%;      Pred. No. 3.3e-50;
Matches 239;      Conservative      0;      Mismatches 81;      Indels 0;      Gaps 0;

```

RESULT	9	
AW405309		
LOCUS		
DEFINITION	AW405309	398 bp mRNA
	UI-HF-BLO-ack-G-01-0-UI.r1	NIH_MGC_37 Homo sapiens cDNA clone
	IMAGE:3059305	5', mRNA sequence.
ACCESSION	AW405309	
VERSION	AW405309.1	GI:6924366
KEYWORDS	EST.	

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward

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FEATURES
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    seq primer: M13 forward.
      Location/Qualifiers
        1..398
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /clone="IMAGE:3059305"
          /clone_lib="NIH_MGC_37"
          /tissue_type="lymph"
          /cell_type="germinal center B cells"
          /cell_line="MGC85"
          /lab_host="DH10B (UTI)"
          /note="Vector: p7713-Pac; Site_1: NotI; Site_2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Ronaldo, Ph.D. and M. Bento Soares, Ph.D."
        88 a 123 c 98 g 89 t
BASE COUNT
ORIGIN
Query Match 58.8% Score 188.8 DB 115 Length 398

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Query Match	58.8%;	Score	188.8;	DB	115;	Length	398;
Best Local Similarity	74.4%;	Pred.	No. 9.8e-50;				
Matches	238;	Conservative	0;	Mismatches	82;	Indels	0;
Gaps	0;						

QY	1	GATATTGTCGCTAACTCAGTCTCCAGCCACCCTGCTGTGTGACACCCAGGAGATACGTCAGT	60
DB	44	GAAATTGTTGTACACAGTCTCCAGCCACCCTGCTTTGTCCTCAGGGGAAGAGCCACC	103
QY	61	CTTTCTCCAGGCCAGCCAAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA	120
DB	104	CTCTCTCGCAGGGCCAGCTCAGAGTGTTAGCAGCTACTTACGCTGGTACCAACAGAAACCT	163
QY	121	CATGAGTCTCCAGGGCTTCATCAAGTATCTGTTCCAGTCCATCTCTGGGATCCCGTCC	180
DB	164	GGCCAGGCTCCCAGGGCTCTCATCTCTGATGTCATCCAAAGGGCCACTGGCATCCCGCC	223
QY	181	AGGTTACGTGCGCATGGATCAGGACGAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT	240
DB	224	AGGTTACGTGGCATGGGTCTGGACAGAGTTCACCTCTACCATCAGCAGCCCTAGAGCCT	283
QY	241	GAAGATTTTGGAAATGTATTTCTGTCAACAGAGTGGCAGCTGGCGCTCACACGTTTCGGAGGG	300
DB	284	GAAGATTTTCGATTTATTACTGTCCACAGCTAGCAACTGGCGCTTGGAGCTTCGCGCCAA	343
QY	301	GGGACCAAGCTGGAAATTAA	320
DB	344	GGGACCAAGGTGGAAGTCAA	363

RESULT	10
AW404697	
LOCUS	AW404697 465 bp mRNA EST 16-FEB-2000
DEFINITION	UI-HF-BLO-acd-b-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE	IMAGE:3058518 5', mRNA sequence.
ACCESSION	AW404697

```

VERSION      AW404506.1  GI:6923754
KEYWORDS     EST.
SOURCE       Homo sapiens
ORGANISM     human.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 465)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              CDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Ronaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      108 a 139 c 115 g 103 t

Query Match      58.3%; Score 187.2; DB 115; Length 465;
Best Local Similarity 74.1%; Pred. No. 3.4e-49;
Matches 237; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY  1  GATATTGCTGAAGTCTCCAGCCAGTCTGTGTGACACAGGAGATAGCGTCAGT 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   85  GAAATAGTGATGAGCGAGTCTCCAGCCAGTCTGTGTGTCCTCCAGGGGAAAGAGCCACC 144

QY  61  CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACATGGTATCAACAAATCA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   145  CTCTCTGCGAGGGCCAGTCAGAGTGTAGCAACAACCTAGCCTGGTACCAAGCAACCT 204

QY  121  CATGAGTCTCCAGGCTTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   205  GGCAGGCTCCAGGCTTCATCTATGTTGGTGCATCCACAGGGCCACTGGTATCCCGACC 264

QY  181  AGGTTAGTGGCAGTGGATCAGGACAGATTCGCTCTCAGTATACACATGTGGAGACT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   265  AGGTTAGTGGCAGTGGTCTGGACAGAGTTCACCTCTCACCATCAGCAGCATGCACTCT 324

QY  241  GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCAGTGGCTTCACAGCTTCGGAGGG 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   325  GAAGATTTTTCAGTTTATTACTGTACAGATATAAATAACTGGCTCTCACTTTTCGGCGGA 384

QY  301  GGGACCAAGCTGGAAATTA 320
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   385  GGGACCAAGCTGGAGATCAA 404

RESULT 11
LOCUS      AW404506
DEFINITION UI-HF-BL0-aby-a-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone

IMAGE:3058065 5', mRNA sequence.
AW404506
EST.
KEYWORDS     EST.
SOURCE       Homo sapiens
ORGANISM     human.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 468)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              CDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source            1..468
                     /organism="Homo sapiens"
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                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Ronaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      106 a 137 c 114 g 111 t

Query Match      58.3%; Score 187.2; DB 115; Length 468;
Best Local Similarity 74.1%; Pred. No. 3.4e-49;
Matches 237; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY  1  GATATTGCTGAAGTCTCCAGCCAGTCTGTGTGACACAGGAGATAGCGTCAGT 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   41  GAAATAGTGATGAGCGAGTCTCCAGCCAGTCTGTGTGTCCTCCAGGGGAAAGAGCCACC 100

QY  61  CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACATGGTATCAACAAATCA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   101  CTCTCTGCGAGGGCCAGTCAGAGTGTAGCAGTACTTAGCCTGGTACCAAGCAACCT 160

QY  121  CATGAGTCTCCAGGCTTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   161  GGCAGGCTCCAGGCTTCATCTATGATGCATCCACAGGGCCACTGGCATCCCGACC 220

QY  181  AGGTTAGTGGCAGTGGATCAGGACAGATTCGCTCTCAGTATACACATGTGGAGACT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   221  AGGTTAGTGGCAGTGGTCTGGACAGAGTTCACCTCTCACCATCAGCAGCCCTAGACCT 280

QY  241  GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCAGTGGCTTCACAGCTTCGGAGGG 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   281  GAAGATTTTTCAGTTTATTACTGTACAGATATAAATAACTGGCTCTCACTTTTCGGCGGA 340

QY  301  GGGACCAAGCTGGAAATTA 320
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   341  GGGACCAAGCTGGAGATCAA 360

RESULT 12
LOCUS      AW404506
DEFINITION UI-HF-BL0-aby-a-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
```


Search completed: October 11, 2001, 14:34:05
Job time: 5542 sec

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XX


```
XX KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW complementarity determining region; ss.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX CDS 1..381
XX FT /*tag= a
XX FT misc_feature 19
XX FT /*tag= b
XX FT /label= MKL104
XX FT misc_feature 385..429
XX FT /*tag= c
XX FT /label= MJK124
XX PN W09412661-A.
XX XX
XX PD 09-JUN-1994.
XX PF 25-NOV-1993; 93WO-JP01724.
XX PR 28-NOV-1992; 92JP-0341255.
XX PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
XX PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
XX DR WPI; 1994-200288/24.
XX DR P-PSDB; AAR54093.
XX XX
XX PT Feline monoclonal antibody and recombinant antibodies specific
XX PT for FHV-1 - for detection, treatment and prevention of FHV-1
XX PT infection.
XX PS Disclosure; Page 18-19; 53pp; Japanese.
XX XX
XX CC The inventors claim a monoclonal antibody against feline herpes
XX CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
XX CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
XX CC used in the detection, treatment and prevention of FHV-1. The
XX CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
XX CC antibody are given in AAR54092. The sequences of the CDRs in the VL of
XX CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR
XX CC sequences are claimed.
XX SQ Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;

Query Match 92.2%; Score 296; DB 15; Length 381;
Best Local Similarity 95.3%; Pred. No. 4.7e-87;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTGAAGTCTCAGTCTCCAGCACCTGCTGTGACACGAGATAGCGTCAGT 60
DB 61 gatattgtctaactcagtcctcagccaccctgtctgtgactcagagatagcgtcagt 120
QY 61 CTTTCTGCGCCAGGCCAGCAAGTATTAGCAACACCTACACTGCTATCAACAAATCA 120
DB 121 cttctctgcggggccagcagaagcattagcaaacacctacactggtatcaacaaaaatca 180
QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180
DB 181 catgagtcctcaagcttcatacgaatgcttccagctcatctctggtatccctcc 240
QY 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240
DB 241 aggttcagtggtgagtcagggacagatttcactctcagtatcaacagtggtgagact 300
QY 241 GAAGATTTGGAATGTTATTTCTGTCACAGAGTGGCAGTGGCTTCACAGCTTCGGAGGG 300
DB 301 gaagattttggaattgtatttctgtcaacagagtaaacagctggcctcacacgttcggtgct 360
```

```
QY 301 GGGACCAAGCTGGAATTA 320
DB 361 gggaccaagctggagctgaa 380

RESULT 4
AAF58747
ID AAF58747 standard; cDNA; 381 BP.
XX AC AAF58747;
XX AC AAF58747;
XX DT 30-APR-2001 (first entry)
XX DE Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.
XX KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX KW light chain; graft versus host disease; transplant; autoimmune disease;
XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;
XX SS.
XX OS Mus SP.
XX PN US6180370-B1.
XX PD 30-JAN-2001.
XX PF 07-JUN-1995; 95US-0484537.
XX PR 28-DEC-1988; 88US-0290975.
XX PR 13-FEB-1989; 89US-0310252.
XX PR 28-SEP-1990; 90US-0590274.
XX PR 19-DEC-1990; 90US-0634278.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Queen CL, Selick HE;
XX DR WPI; 2001-190856/19.
XX DR P-PSDB; AAB69687.
XX XX
XX PT Producing humanized immunoglobulin, involves producing a cell
XX PT containing DNA segments encoding humanized heavy and light chain
XX PT variable regions, and expressing the DNA segments in the cell -
XX PS Example 8; Fig 39; 145pp; English.
XX XX
XX CC The present invention describes a method of producing humanised
XX CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX CC humanised version of an immunoglobulin. This is obtained by comparing a
XX CC donor and human immunoglobulin and producing a combined antibody which
XX CC contains part of each. These are useful in the treatment of
XX CC graft-versus-host disease, transplant rejection, autoimmune diseases such
XX CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
XX CC and systemic lupus erythematosus, herpes infections, CMV virus infections
XX CC and myeloid leukaemia. The present sequence is an antibody cDNA used to
XX CC demonstrate the method of the invention.
XX SQ Sequence 381 BP; 97 A; 92 C; 89 G; 103 T; 0 other;

Query Match 92.2%; Score 296; DB 22; Length 381;
Best Local Similarity 95.3%; Pred. No. 4.7e-87;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTGAAGTCTCAGTCTCCAGCACCTGCTGTGACACGAGATAGCGTCAGT 60
DB 61 gatattgtctaactcagtcctcagccaccctgtctgtgactcgggagatagcgtcagt 120
QY 61 CTTTCTGCGCCAGGCCAGCAAGTATTAGCAACACCTACACTGCTATCAACAAATCA 120
DB 121 cttctctgcagggccagcagaagattagcaaacacctacactggtatcaacaaaaatca 180
```

QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGGATCCCTCC 180
 Db 181 catgagtcctccaaaggcttctcatcaagtagctctccagtcctctcggatccctcc 240
 QY 181 AGTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGTGGAGACT 240
 Db 241 aggttcagtgagtgatcaggagacagatttcactctcagtgccaagtggtgagact 300
 QY 241 GAAGATTTTGGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
 Db 301 gaagattttgggaatgtattttctgtcaacagagtaaacagttggcctcactacgttcggaagg 360
 QY 301 GGGACCAAGCTGGAATTA 320
 Db 361 gggaccaagctggaataaa 380

RESULT 5
 AAQ04654
 ID AAQ04654 standard; DNA; 5238 BP.
 AC AAQ04654;
 XX
 DT 01-OCT-1990 (first entry)
 XX
 DE Plasmid pBT111 encoding antibody MAK33 kappa chain.
 XX
 KW Antibody MAK33; kappa chain; plasmid pBT111; activated antibody; ss.
 XX
 FH Key Location/Qualifiers
 CDS 7..663
 FT /*tag= a
 FT /product= kappa chain of MAK33
 XX
 DE DE3835350-A.
 XX
 PD 19-MAR-1990.
 XX
 PF 17-OCT-1988; 88DE-3835350.
 XX
 PR 17-OCT-1988; 88DE-3835350.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Rudolph R, Buchner J, Lenz H;
 XX
 DR WPI; 1990-156813/21.
 XX
 PT Activated antibody prodn. from recombinant procarvotic cells -
 PT by solubilisation under reducing conditions, then oxidative
 PT renaturation, carried out at low protein concn.
 XX
 PS Disclosure; ; p; German.
 XX
 CC Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding
 CC the fd chain of antibody MAK33 were used to transform E.coli DSM 3689
 CC and the resulting cells grown to form inclusion bodies. After the final
 CC renaturation step an 18% yield of biologically-active protein was
 CC produced.
 CC see also AAQ04655.
 XX
 SQ Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;

Query Match 90.2%; Score 289.6; DB.11; Length 5238;
 Best Local Similarity 94.1%; Pred. No. 1.7e-84;
 Matches 301; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GATATTGTGCTAACTAGTCTCCAGCCACCCCTGTGTGACACACGAGATAGCCTCAGT 60
 Db 7 gatattgtgctaactcagtcctccagccaccctgtgtgactccaagagatagcgtcagt 66
 QY 61 CTTTCTCGCCAGGCCCAAGATATTAGCAACACCCTACACTGTGTATCAACAAAAATCA 120

Db 67 ctttctcaggggccagcaaaagtattagcaaaccttacactgtatcaacaaaatca 126
 QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
 Db 127 catgagtcctccaaaggcttctcatcaaatatgcttccagtcctctcggatccctct 186
 QY 181 AGTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGTGGAGACT 240
 Db 187 aggttcagtgagtgatcaggagacagatttcactctcagtcatacaacagtggtgagact 246
 QY 241 GAAGATTTTGGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
 Db 247 gaagattttgggaatgtattttctgtcaacagagtaaacagctggcctctcagctcgtggtgct 306
 QY 301 GGGACCAAGCTGGAATTA 320
 Db 307 gggaccaagctggagctgaa 326

RESULT 6
 AAZ35242
 ID AAZ35242 standard; cDNA; 381 BP.
 AC AAZ35242;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Mouse anti-verotoxin II antibody VTml-1 VL cDNA.
 XX
 KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
 KW monoclonal antibody; light chain; mouse; humanised antibody;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 KW HUS; therapy; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 sig_peptide 1..60
 FT /*tag= a
 FT mat_peptide 58..381
 FT /*tag= b
 FT /trans_except= (pos:184..186, aa:Lys)
 XX
 PN WO9959629-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 19-MAY-1999; 99WO-US11179.
 XX
 PR 20-MAY-1998; 98US-0086570.
 XX
 PA (TEIJ) TEIJIN LTD.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
 XX
 DR WPI; 2000-086580/07.
 DR P-PSDB; AAY32405.
 XX
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli -
 XX
 PS Disclosure; Fig 1b; 59pp; English.
 XX
 CC This DNA sequence codes for the light chain variable region (see
 CC AAY32405) of murine monoclonal antibody VTml-1 (MuVTml-1), an
 CC antibody that specifically binds to the B subunit of verotoxin II
 CC (VT2). The invention relates to humanised antibodies against VT2
 CC that are capable of neutralizing VT2 and/or VT2 variants. The
 CC humanised antibody is a humanized form of MuVTml-1 comprising the
 CC complementarity determining regions of MuVTml-1 and heavy and
 CC light chain variable region frameworks from the human GF4 antibody

CC heavy and light chain frameworks, provided that at least 1 position
 CC selected from L49, H29, H30, H49 and H98 is occupied by the amino
 CC acid at the equivalent position of the MuVtm1-1 antibody heavy or
 CC light chain variable region framework. Such humanized antibodies
 CC (see AAV32406-07) have an affinity for VT2 that is 3-, 5 or 10-times
 CC that of MuVtm1-1. They are used for treating a patient suffering
 CC from, or at risk of, the toxic effects from VT2 (claimed), especially
 CC for treating verotoxin producing Escherichia coli (VTEC) infection,
 CC and haemolytic uraemic syndrome (HUS).
 XX
 SQ Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;

Query Match 88.2%; Score 283.2; DB 21; Length 381;
 Best Local Similarity 92.8%; Pred. No. 7.1e-83;
 Matches 297; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 GATATTGTGCTTAAGTCTCCAGCCAGCCCTGCTGTGACACCAGGAGTAGCGTCAGT 60
 DB 61 gatgtgtgcttaagctctccagccagccctgtctgtgactccagagatagcgtcagt 120
 QY 61 CTTTCTCCAGCCAGCCAGCCAGGATTAAGCAACCCAGCTGCTATCAACAAAATCA 120
 DB 121 ctttctcagggccagcttaagcaactattagcaaacctacactgtatcaacaaatca 180
 QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGCTGTTCCAGTCCATCTCTGGATCCCTCC 180
 DB 181 catgagctcacaaggctctcatcaagctgcttccagccatctctggtatccctcc 240
 QY 181 AGGTTGAGTGGCAGTGCATGAGGACAGATTCGCTCTCAGTATCAACAGTGGAGACT 240
 DB 241 aggttcagtgagtgatcagggacagatttccactcagtcagtcacagtggtgaact 300
 QY 241 GAAGATTTTGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
 DB 301 gaagattttgaatgtattctgtcaacagagttacagctggccgctcagcttcggtct 360

QY 301 GGGACCAAGCTGGAATTA 320
 DB 361 gggaccaagctggagctgaa 380

RESULT 7
 AAV71798
 ID AAV71798 standard; cDNA; 324 BP.

AC AAV71798;
 XT 15-MAR-1999 (first entry)
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL cDNA.
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.
 XX Mus sp.
 OS
 XX W09840488-A1.
 PN
 PD 17-SEP-1998.
 XX
 PF 12-MAR-1998; 98WO-US04987.
 XX
 PR 12-MAR-1997; 97US-0039609.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johanson KO, Jonak ZL, Taylor AH;
 XX

DR WPI; 1998-034590/03.
 DR P-PSDB; AAW84094.
 XX
 PT New anti alpha.v beta.3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Example 13; Page 59-60; 97pp; English.

CC This cDNA sequence codes for the light chain variable region (VL,
 CC see AAW84094) of the anti-human alpha-v beta-3 vitronectin receptor
 CC murine monoclonal antibody D12. It was obtained from hybridoma
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers
 CC (see AAV71808-09). A heavy chain variable region clone (see AAV71797)
 CC has also been identified. D12 VH and VL show sequence similarity
 CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
 CC AAW84098) were constructed by combining the framework regions of the
 CC human V region consensus sequences with complementarity determining
 CC regions of D12 (keeping some preferred murine framework residues).
 CC The humanised antibodies are specifically reactive with the human
 CC alpha-v beta-3 protein receptor and capable of neutralising the
 CC receptor. They can be used for passive immunotherapy of a disorder
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 CC disorders or angiogenic-related disorders, such as angiogenesis
 CC associated with diabetic retinopathy, atherosclerosis and
 CC restenosis, chronic inflammatory disorders, macular degeneration,
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
 CC diseases where bone resorption is associated with pathology such as
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone
 CC loss due to immobilisation or sex hormone deficiency. They can also
 CC be used for targeted drug therapy, and for detection and diagnosis.
 XX
 SQ Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;

Query Match 87.2%; Score 280; DB 20; Length 324;
 Best Local Similarity 92.2%; Pred. No. 7.4e-82;
 Matches 295; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GATATTGTGCTTAAGTCTCCAGCCAGCCCTGCTGTGACACCAGGAGTAGCGTCAGT 60
 DB 1 gatattgtgtcactcagctctccagccacctgtgtgactccagagatagcgtcagt 60
 QY 61 CTTTCTCCAGCCAGCCAGCCAGGATTAAGCAACCCAGCTGCTATCAACAAAATCA 120
 DB 61 ctttctcagggccagccagccagcttattagcaaccacctacactggtatcaacaagatca 120
 QY 121 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGATCCCTCC 180
 DB 121 catgagctccaaggcttctcatcaagtagcttccagctcattctctggatccctcc 180
 QY 181 AGGTTGAGTGGCAGTGCATGAGGACAGATTCGCTCTCAGTATCAACAGTGTGGAGACT 240
 DB 181 aggttcagagcagtgatcagggacagatttccactcactcactcaatcaacatttggagact 240
 QY 241 GAAGATTTTGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
 DB 241 gagattttggaatgtattctgtcaacagagtaacagctggcccttccagcttcggtctc 300
 QY 301 GGGACCAAGCTGGAATTA 320
 DB 301 gggaccaagctggaaataaa 320

RESULT 8
 AAT33446
 ID AAT33446 standard; cDNA; 324 BP.
 XX
 AC AAT33446;
 XX

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DT 22-NOV-1996 (first entry)
XX EGF receptor chimeric MAb chMint5 VL chain cDNA.
DE
XX Mouse-human chimeric antibody; monoclonal antibody; chMint5;
KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
KW immunotoxin; immunocytokine; tumour; cancer; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT misc_feature 1..24
FT /*tag= a
FT /note= "primer-derived sequence"
FT misc_feature 301..324
FT /*tag= b
FT /note= "primer-derived sequence"
FT
XX
PN WO9627010-A1.
XX
XX 06-SEP-1996.
XX
XX 01-MAR-1996; 96WO-EP00805.
XX
XX 01-MAR-1995; 95IT-OfI0036.
XX
XX (ITU-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
XX
XX Anastasi AM, Colnaghi MT, De Santis R, Di Massimo AM;
PI Ferrer Marsal C, Mele A;
XX
XX WPI; 1996-412776/41.
DR P-PSDB; AAW0241.
XX
XX Murine/human chimeric monoclonal antibody, chMint5 specific for
PT EGF-R - shows a lower immunogenicity when administered to humans
XX
XX Claim 6; Page 17; 28pp; English.
XX
XX A cDNA clone (AA733446) codes for the light chain variable region (VL)
CC (AAW0241) of the epidermal growth factor receptor (EGF-R)-specific
CC mouse-human chimeric antibody chMint5. VH and VL chain sequences
CC were obtd. by PCR amplification of RNA from murine Mint5 hybridoma
CC DSM ACC2150 and fused to human C-gamma and CK genes. Constructs
CC were expressed in CHO cell transfectants. chMint5 shows lower
CC immunogenicity than Mint5 when administered to humans. It can be
CC used in diagnostic assays or used to produce immunotoxins or
CC immunocytokines useful for tumour therapy.
XX
XX Sequence 324 BP; 85 A; 83 C; 78 G; 78 T; 0 other;
SQ

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Query Match 85.2%; Score 273.6; DB 17; Length 324;
Best Local Similarity 90.9%; Pred No. 9, 1e-80;
Matches 291; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 GATATTGCTCACTCAGTCCAGCCACCCCTGCTGTGACACCCAGGAGATAGCCTCAGT 60
Db 1 gacatcagctgacccagctccagccaccctgtctgtgactccagagatagctcagt 60
QY 61 CTTTCTGCGCAGCCAGCAAGATTATGACACACCCCTACACTGGTATCAACAAATCA 120
Db 61 cttctctgtagggccagcaagattatgacacagcagctcactggtatcaacaaatca 120
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTCCAGTCCATCTCTGGATCCCTCC 180
Db 121 catgagctcccaaggcttctcatcaagtagtctccagtcctctctggtggtccctcc 180
QY 181 AGGTTCAGTGGCAGTGGATCAGGAGAGATTTCGCTCTCAGTATCAACAGTGTGGAGCT 240
Db 181 aggttcagcgagtgatcagggacagatcttcaactctcaactatcaacagtgtagact 240
QY 241 GAAGATTTGGGAATGTAATTTCTGTCAACAGAGTGGCAGCTGCCTCACACGTTCCGAGGG 300

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Db 241 aaagattttggaatgtattctgtcaacagagtgcacagttggcagcttgcgttgga 300
QY 301 GGCACCAAGCTGGAATTA 320
Db 301 gggaccaagctggatcaaa 320

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RESULT 9
AAV49821
ID AAV49821 standard; DNA; 321 BP.
XX
AC AAV49821;
XX
DT 02-NOV-1998 (first entry)
XX
DE Vitaxin antibody light chain variable region DNA.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT /*tag= a
FT /product= "vitaxin antibody light chain variable region"
FT /note= "partial sequence, no start or stop codon given"
FT
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
DR P-PSDB; AAW76002.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 6; Fig 1b; 129pp; English.
XX
XX This sequence encodes the vitaxin antibody variable light chain region.
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ

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Query Match 83.6%; Score 268.2; DB 19; Length 321;
Best Local Similarity 89.7%; Pred No. 5, 2e-78;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Db	334	gagagtggtgagtggtattactgtcaaaatggtcacagctttccgtacacgttcgaggg	393
Qy	301	GGGACCAAGCTGGAAATTA 320	
Db	394	gggaccaagctggaataaa 413	
RESULT 13			
AAF28199			
XX	ID	AAF28199 standard; DNA; 321 BP.	
AC	AAF28199;		
XX	03-APR-2001	(first entry)	
XX	DNA encoding light chain variable region of LM609.		
XX	LM609;	grafted antibody; alphaVbeta_3 integrin; angiogenesis;	
KW	inflammatory; cancer; retina; restenosis; osteoporosis; ds.		
XX	Unidentified.		
OS	WO200078815-A1.		
XX	28-DEC-2000.		
XX	23-JUN-2000;	2000WO-US17454.	
XX	24-JUN-1999;	99US-0339922.	
PR	(MOLE-) APPLIED MOLECULAR EVOLUTION.		
XX	Huse WD, Wu H;		
XX	WPI; 2001-050110/06.		
XX	Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -		
XX	Disclosure; Fig 7; 132pp; English.		
XX	The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of		
CC	alphavbeta_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis.		
XX	Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;		
Qy	Query Match	82.6%;	Score 265.2; DB 22; Length 321;
XX	Best Local Similarity	88.8%;	Pred. No. 5e-77;
XX	Matches 285; Conservative	0; Mismatches 36; Indels 0; Gaps	
Qy	1	GATATTGCTGAAGTCACTCAGTCTCCAGCCACCCTGCTCTGTGCACACCAGGAGATAGCGTCAGT	60
Db	1	gagatgtgtctaactcagttccagccacctgtctctcagccctgtctcagccgaggagaaagggcgact	60
Qy	61	CTTTCTCTGCCAGCCGCCAAAGTATTAGCAACCACTACTGGTGATCAACAAAAATCA	120
Db	61	ctttctgcaggccagcaagattagcaaccctacctggtatatacaaaaggcct	120
Qy	121	CATGAGTCTCCAAGGTTCTCAATCAAGTATGTCCTCCAGTCCATCTCTGGGATCCCCCTCC	180

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Query Match      80.7%; Score 259.2; DB 20; Length 8858;
Best Local Similarity 88.1%; Pred. No. 1.8e-74;
Matches 282; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GATATTGTCTTAACCTCAGTCTCCAGCCACCCTGTCTGTGACACACGAGGATAGCGTCAGT 60
DB 1065 gacattgttctgactcagctctccagccaccctgtctgtgactccaggagatagagctct 1124
QY 61 CTTTCTCGCAGCCAGCCAAAGATTATTAGCAACCCACTACACTGGTATCAACAAAAATCA 120
DB 1125 cttctcagggccagcagagattagcactactacactggtatcaacaaaaatca 1184
QY 121 CATGAGTCTCCAGGCTTCTCAATCAAGTATGCTTCCCATCTCCATCTCGGATCCCTCC 180
DB 1185 catgagctccagggcttctcaaatatgttccacttccatctctggatccctcc 1244
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGGAGACT 240
DB 1245 aggttcagtgccagtggtcaggtcagatttccactctcagtcatacaacagtggaacct 1304
QY 241 GAAGATTTGGGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCCGGAGG 300
DB 1305 gaagatgttggaaattattactgtcaaatggtcacagctttccgtggagcttcggtgga 1364
QY 301 GGGACCAAGCTGGAAATTA 320
DB 1365 ggcaccaagctggaataca 1384

RESULT 15
ID AAT38510
AC AAT38510;
XX 23-JUN-1997 (first entry)
XX Light chain coding sequence of monoclonal antibody 4B4-1-1.
KW Antibody; human; heavy chain; variable region; light chain; MAb; 4-1BB;
KW tumour necrosis factor receptor; membrane protein; accessory molecule;
KW T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;
KW immunosuppressive agent; autoimmune disease; rejection response; therapy;
KW organ transplantation; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_feature 1..324
FT /*tag= a
FT /*note= "claimed light chain variable region coding
FT sequence"
FT misc_feature 325..363
FT /*tag= b
FT /*note= "constant region (encoded protein not given in
FT specification)"
XX WO9632495-A1.
XX 17-OCT-1996.
XX 06-APR-1996; 96WO-KR00045.
XX 08-APR-1995; 95KR-0008176.
XX (GLDS ) LG CHEM LTD.
XX Kang CY, Kim JG;
XX WPI; 1996-477145/47.
XX P-PSDB; AAW04333.
XX Monoclonal antibody specific for human 4-1BB - useful as
```

```
PT immunospecific agent for treating autoimmune diseases and preventing
PT organ transplant rejection
XX Claim 4; Fig 3a; 37pp; English.
XX AAT38509 and AAT38510 represent the coding sequences for the variable
CC regions of the heavy and light chains of the antibody of the invention.
CC This sequence is stated in the specification as being 372 bp in length,
CC but only comprises 363 bp. The antibody of the invention (designated
CC 4B4-1-1) is a monoclonal antibody (MAb) specific for human 4-1BB. 4-1BB
CC encodes a member of the tumour necrosis factor receptor family of
CC integral membrane proteins. 4-1BB is an accessory molecule expressed on
CC the surface of T-cells in the initial stage of activation. The accessory
CC molecules on the T-cell bind to the corresponding ligand on the
CC antigen-presenting cell and this accelerates the activation of the T- and
CC antigen-presenting cells, thereby promoting various immune responses. The
CC MAb is specific for human 4-1BB, which is selectively expressed on
CC activated T-cells. The MAb is useful as an immunosuppressive agent. It
CC can be used for the treatment of autoimmune diseases, such as rheumatoid
CC arthritis, and for preventing rejection response after organ
CC transplantation.
XX Sequence 363 BP; 91 A; 102 C; 79 G; 91 T; 0 other;
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Query Match      79.8%; Score 256; DB 17; Length 363;
Best Local Similarity 87.5%; Pred. No. 5.3e-74;
Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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DB 1 gacattgtgactgacccagctctccagccaccagctgtgactccaggagatagagctct 60
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DB 61 cttctcagggccagcagagattagcactactacactggtcactcagtcatacaaaaaatca 120
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCCATCTCTCGGATCCCTCC 180
DB 121 catgagctccagggcttctcactcaaatatgcttcccaatccatctctggatccctcc 180
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGGAGACT 240
DB 181 aggttcagtgccagtggtcaggtcagatttccactctcagtcatacaacagtggaacct 240
QY 241 GAAGATTTGGGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCCGGAGG 300
DB 241 gaagatgttggagtggtattactgtcaaatggtcacagctttccctccagcttcggtgga 300
QY 301 GGGACCAAGCTGGAAATTA 320
DB 301 ggcaccaagctggaataca 320
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Search completed: October 11, 2001, 15:12:39
Job time: 6471 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:14 ; Search time 87.94 Seconds
(without alignments)
891.027 Million cell updates/sec

Title: US-08-791-391A-7

Perfect score: 321

Sequence: 1 GATATTGTGCTAACTCACTC.....GGACCAAGCTGGAAATTAG 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	92.2	381	1	US-07-634-278-82
2	296	92.2	381	1	US-08-477-728-82
3	296	92.2	381	1	US-08-474-040-82
4	296	92.2	381	1	US-08-487-200-82
5	296	92.2	381	4	US-08-484-537-82
6	296	92.2	424	1	US-08-436-463-3
7	289.6	90.2	5238	6	5453363-1
8	256	79.8	324	2	US-08-737-560A-13
9	256	79.8	363	2	US-08-737-560A-8
10	230.4	71.8	322	2	US-08-476-176B-3
11	230.4	71.8	322	3	US-08-127-721A-3
12	230.4	71.8	322	3	US-08-485-246A-3
13	224	69.8	321	2	US-08-232-081B-39
14	219.4	68.3	318	1	US-08-326-362-3
15	218.8	68.2	318	2	US-08-800-198-3
16	218.8	68.2	318	3	US-09-296-595-3
17	218.8	68.2	720	2	US-08-800-198-7
18	218.8	68.2	720	3	US-09-296-595-7
19	216	67.3	720	2	US-07-956-399-1
20	212.2	66.1	429	2	US-08-653-402B-7
21	211.2	65.8	717	2	US-07-956-399-3
22	209.6	65.3	321	1	US-08-192-102-2
23	209.6	65.3	321	1	US-08-324-799-2
24	209.6	65.3	321	2	US-08-192-861A-2
25	196.8	61.3	321	2	US-08-232-081B-35
26	193.6	60.3	321	2	US-08-232-081B-36
27	174.8	54.5	812	1	US-08-053-131-178

Sequence 178, App
Sequence 41, Appl
Sequence 19, Appl
Sequence 201, App
Sequence 180, App
Sequence 43, Appl
Sequence 216, App
Sequence 107, App
Sequence 113, App
Sequence 199, App
Sequence 211, App
Sequence 218, App
Sequence 102, App
Sequence 105, App
Sequence 109, App
Sequence 31, Appl
Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-07-634-278-82

Query Match          92.2%; Score 296; DB 1; Length 381;
Best Local Similarity 95.3%; Pred. No. 2e-89;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db 61 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACCTCCGGAGATAGCGTCAGT 120
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QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGGATCCCTCC 180
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QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240
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Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 300
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QY 241 GAAGATTTTGGAAATGATTTCTGTCAACAGAGTGGCGCTCACAGTTCGGAGGG 300
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Db 301 GAAGATTTTGGAAATGATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTTCGGAGGG 360
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QY 301 GGGACCAAGCTGGAATATA 320
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Db 361 GGGACCAAGCTGGAATATA 380
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RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match          92.2%; Score 296; DB 1; Length 381;
Best Local Similarity 95.3%; Pred. No. 2e-89;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60
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QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCCACTACCTGGTATCAACAAAAATCA 120
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QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGGATCCCTCC 180
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QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240
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Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 300
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QY 301 GGGACCAAGCTGGAATATA 320
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Db 361 GGGACCAAGCTGGAATATA 380
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RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-474-040-82

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Query Match	92.2%	Score 296;	DB 1;	Length 381;
Best Local Similarity	95.3%;	Pred. No. 2e-89;		
Matches 305;	Conservative	0;	Mismatches 15;	Indels 0;
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QY	61	CTTTCCTGCCAGGCCGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAAAAATCA	120	
Db	121	CTTTCCTGCCAGGCCGCCAAAGTATTAGCAACAACCTACACTGGTATCAACAAAAATCA	180	
QY	121	CATGAGTCTCAAGGCTTCATCAAGATATGTTCCAGTGCATCTCTGGGATCCCCTCC	180	
Db	181	CATGAGTCTCAAGGCTTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCCTCC	240	
QY	181	AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT	240	
Db	241	AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTGTCAACAGGTTGTGGAGACT	300	
QY	241	GAAGATTTTGGATGTATTCTGTCAACAGAGTGGCAGCTGGCCCTCAACAGCTTCGGAGGG	300	
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Db	361	GGGACCAAGCTGGAAATTA	380	

RESULT 4
US-08-487-200-82
; Sequence 82, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.

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: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,200
: FILING DATE: 7-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/634,278
: FILING DATE: 19-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002610
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 381 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..381
: US-08-487-200-82

Query Match 92.2%; Score 296; DB 1; Length
Best Local Similarity 95.3%; Pred. No. 2e-89;
Matches 305; Conservative 0; Mismatches 15; Index

Qy 1 GATATTGTGTAAGTCTCAGTCTCCAGCCACCCTGTCTGTGACACACACGAGGAGG
Db 61 GATATTGTGTAAGTCTCAGTCTCCAGCCACCCTGTCTGTGACTCCGGGATATC
Qy 61 CTTTCCTGCCAGGCCACCCAAAGTATTAGCAACCACTACATCGGTATCATC
Db 121 CTTTCCTGCCAGGCCACCCAAAGTATTAGCAACCACTACATCGGTATCATC
Qy 121 CATGAGTCTCGAAGGCTTCTCATCAAGTATGCTTCCAGTCCCACTCTGTCG
Db 181 CATGAGTCTCGAAGGCTTCTCATCAAGTATGCTTCCAGTCCCACTCTGTCG
Qy 181 AGGTTCAAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAC

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Db 241 AGTTTCAGTGGCAGTGCATCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
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Db 301 GAAGATTTTGGGATGATTTCTCTCAACAGAGTAAACAGTTGGCCTCATACGTTTCGGAGGG 360
QY 301 GGGACCAAGCTGGAATAAA 320
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 5
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-484-537-82

Query Match 92.2%; Score 296; DB 4; Length 381;
Best Local Similarity 95.3%; Pred. No. 2e-89;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 GATATGTGCTAACTACAGTCTCCAGCCAGCCCTGCTCTGTGACACCAGGAGATACCGTCAGT 60
Db 61 GATATGTGCTAACTACAGTCTCCAGCCAGCCCTGCTCTGTGACCCGGGAGATAGCGTCAGT 120
QY 61 CTTTCTCGCCAGGCCAGCCAAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAATCA 120
Db 121 CTTTCTCGCCAGGCCAGCCAAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAATCA 180
QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180
Db 181 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240
QY 181 AGSTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240
Db 241 AGSTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
QY 241 GAAGATTTTGGGATGATTTCTCTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGGG 300
Db 301 GAAGATTTTGGGATGATTTCTCTCAACAGAGTAAACAGTTGGCCTCATACGTTTCGGAGGG 360
QY 301 GGGACCAAGCTGGAATAAA 320
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 6
US-08-436-453-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-EPHILINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YON, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 23..403
US-08-436-463-3

Query Match 92.2%; Score 296; DB 1; Length 424;

Best Local Similarity 95.3%; Pred. No. 2.le-89;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACACAGGAGATAGCGTCAGT 60
DB 83 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACACAGGAGATAGCGTCAGT 142

QY 61 CTTTCCTGCCAGCCGACCAAGATTATAGCAACACCTACACTGGTATCAACAAAAATCA 120

DB 143 CTTTCCTGCCAGCCGACCAAGATTATAGCAACACCTACACTGGTATCAACAAAAATCA 202

QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180

DB 203 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 262

QY 181 AGGTTCAAGTGCAGTGCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240

DB 263 AGGTTCAAGTGCAGTGCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 322

QY 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTGGCAGCTGGCTCAGTATCAACAGTGTGGAGGG 300

DB 323 GAAGATTTTGAATGTATTCTGTCAACAGAGTGGCAGCTGGCTCAGTATCAACAGTGTGGAGGG 382

QY 301 GGGACCAAGCTGGAAATTA 320

DB 383 GGGACCAAGCTGGAGCTGAA 402

RESULT 7

5453363-1

PATENT NO. 5453363

APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; NATTES, RALF

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

ING AFTER GENETIC EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR-1990

APPLICATION NUMBER: 76,207

FILING DATE: 23-OCT-1986

SEQ ID NO: 1:

LENGTH: 5238

5453363-1

Query Match

Best Local Similarity 90.2%; Score 289.6; DB 6; Length 5238;

Matches 301; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACACAGGAGATAGCGTCAGT 60

DB 7 gatattgtctaactcagtcctccagccacctgtctgtgactccaagagatagcgtcagt 66

QY 61 CTTTCCTGCCAGCCGACCAAGATTATAGCAACACCTACACTGGTATCAACAAAAATCA 120

DB 67 ctttcctgagggccagccaaagtattagcaaacactacactggtatcaacaaaaatca 126

QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180

DB 127 catgagtcctcaaggcttcctcataaataatgcttcctcagtcctcctctggtgagtcctct 186

QY 181 AGGTTCAAGTGCAGTGCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240

DB 187 aggttcagtgagcagtgatcagggacagatttcactctcagtatcaacagctgagagact 246
QY 241 GAAGATTTTGAATGTATTCTGTCAACAGAGTGGCAGCTGGCTCAGTATCAACAGCTTGGAGGG 300
DB 247 gaagattttggaatgtattctgtcaacagagataacagctggcctctcaegttcgggtgct 306
QY 301 GGGACCAAGCTGGAAATTA 320
DB 307 gggaccaagctggagctgaa 326

RESULT 8

US-08-737-560A-13

Sequence 13, Application US/08737560A

Patent No. 5928893

GENERAL INFORMATION:

APPLICANT: KANG, Chang-Yuil

APPLICANT: KIM, Joong-Gon

TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN

TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: KANG, Chang-Yuil

STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,

STREET: Kwanak-gu

CITY: Seoul

STATE: Seoul

COUNTRY: Republic of Korea

ZIP: 151-057

ADDRESSEE: KIM, Joong-Gon

STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu

CITY: Seoul

STATE: Seoul

COUNTRY: Republic of Korea

ZIP: 135-110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage

COMPUTER: IBM PC/AT

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,560A

FILING DATE: 13-NOV-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: KR 95-8176

FILING DATE: 08-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 324 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: polynucleotide encoding 4B4-1-1

OTHER INFORMATION: light chain variable region

US-08-737-560A-13

Query Match

Best Local Similarity 79.8%; Score 256; DB 2; Length 324;

Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCTCCAGCCCTGCTGTGTGACACAGGAGATAGCGTCAGT 60

Db 1 GACATTTGTGATGACCCAGTCTCCAGCCAGCTGTGTGACTCCAGGAGATAGAGTCTCT 60
QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTTACCTGGTATCAACAAAAATCA 120
Db 61 CTTTCTGCGAGCCAGCCAGGACTATTACGAGTACTTACCTGGTATCAACAAAAATCA 120
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
QY 181 AGTTTCAGTGGGAGTGGATCAGGAGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
Db 181 AGTTTCAGTGGGAGTGGATCAGGAGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
QY 241 GAAGATTTTGGAGTGGATTTCTGTCACAGAGTGGGAGTGGGCTTCCGAGG 300
Db 241 GAAGATTTTGGAGTGGATTTCTGTCACAGAGTGGGAGTGGGCTTCCGAGG 300
QY 301 GGGACCAAGCTGGAATTA 320
Db 301 GGGACCAAGCTGGAATTA 320

RESULT 9

US-08-737-560A-8
; Sequence 8, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain
; OTHER INFORMATION: variable region
; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1
; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2
; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3
; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region
US-08-737-560A-8

Query Match 79.8%; Score 256; DB 2; Length 363;
Best Local Similarity 87.5%; Pred. No. 4.1e-76;
Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 GATATTGTCTTAACCTCAGTCTCCAGCCAGCTGTGTGACTCCAGGAGATAGAGTCTCT 60
Db 1 GACATTTGTGATGACCCAGTCTCCAGCCAGCTGTGTGACTCCAGGAGATAGAGTCTCT 60
QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTTACCTGGTATCAACAAAAATCA 120
Db 61 CTTTCTGCGAGCCAGCCAGGACTATTACGAGTACTTACCTGGTATCAACAAAAATCA 120
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
QY 181 AGTTTCAGTGGGAGTGGATCAGGAGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
Db 181 AGTTTCAGTGGGAGTGGATCAGGAGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
QY 241 GAAGATTTTGGAGTGGATTTCTGTCACAGAGTGGGAGTGGGCTTCCGAGG 300
Db 241 GAAGATTTTGGAGTGGATTTCTGTCACAGAGTGGGAGTGGGCTTCCGAGG 300
QY 301 GGGACCAAGCTGGAATTA 320
Db 301 GGGACCAAGCTGGAATTA 320

RESULT 10

US-08-476-176B-3
; Sequence 3, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:

```

; NAME: NO. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ. ID NO.: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..321
; OTHER INFORMATION:
; OTHER INFORMATION: domain of murine antibody TES-C21"
;
; US-08-476-176B-3

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Query Match	71.8%;	Score 230.4;	DB 2;	Length 322;
Best Local Similarity	82.5%;	Pred. No. 1.3e-67;		
Matches 264;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps 0;
QY 1	GATATTGCTAACTCAGTCTCCAGCCACCGTGTGTGCACACCAGGAGATAGCGTCAGT	60		
Db				
QY 1	GACATCTGTGACTCAGTCTCCAGCCATCTGTGTGTGATCCAGGAGAAGAGTCTAGT	60		
Db				
QY 61	CTTTCTCTGCCAGGCGCCAAAGTATTAGCAACCACTACACTGGTATCAACAATAATCA	120		
Db				
QY 61	TTCTCTGCGAGGCCAGTCCAGAGATTGGCACAACATACACTGGTATCACCAGAAGACA	120		
Db				
QY 121	CATGAGTCTCCAGGCTTCATCATCAAGTATGGTTCCCGAGTCCATCTCTGGGATCCCCGCC	180		
Db				
QY 121	GATGGTTCTCCAGGCTTCTCATAAAGTATGCTTCTGAGTCTATCTCTGGGATCCCCGCC	180		
Db				
QY 181	AGGTTCACTGGCAGTGGATCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT	240		
Db				
QY 181	AGGTTTAGTGGCAGTGGATCAGGACAGAGTTTACTCTAAACATCAACAGTGTGGAGTCT	240		
Db				
QY 241	GAAGATTTTGGAAATGATTCTGTGCAACAGAGTGGCAGCTGGCCCTCACACCTTCGGAGGG	300		
Db				
QY 241	GAAGATATTCGAGATTATTACTGTCAACAAGTGTAGTGTGCCCAACCACTTCGGAGGG	300		
Db				
QY 301	GGGACCAAGCTGGAAATTA	320		
Db				
QY 301	GGGACCAAGCTGGAGATAA	320		
Db				

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RESULT 11
US-08-127-721A-3
; Sequence 3, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saidanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable
127-721A-3
OTHER INFORMATION: domain of murine antibody TES-C21 "
US-08-127-721A-3

```

Query Match	71.8%;	Score 230.4;	DB 3;	Length 322;
Best local similarity	82.5%;	Pred. No. 1.3e-67;		
Matches 264;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps
QY	1	GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGCTGTCGACACCCAGGAGATACGCGTCACT	60	
DB	1	GACATCTTGCTGACTCAGTCTCCAGCCATCCTGCTGTCGAGTCCAGGAAAGAGTCACT	60	
QY	61	CTTTCTCTCCAGGCCCAGCCAAAGTATTAGCAACACCTACTACCTGGTATCAACAACAAATCA	120	
DB	61	TTCTCTCGCAGGGCCAGTCAGACATTTGGCACAAACATACACTGGTATCAGCAAGAACA	120	
QY	121	CATGAGTCTCCAGGGCTTCATCAAGTATCGTTCCTCCAGTCCATCCTCGGATCCCTCC	180	
DB	121	GATGGTTCTCCAGGGCTTCATCAAAAGTATGCTTCCTGAGTCTATCTCTGGGATCCCTCC	180	
QY	181	AGGTCAGTGGCAGTGGATCAGGAGCAGATTTCGCTCTCAGTATCAACAGTGTGGAGCT	240	
DB	181	AGGTTAGTGGCAGTGGATCAGGAGCAGAGTTTACTCTAAACATCAACAGTGTGGAGCT	240	
QY	241	GAAGATTTTGGATGTATTCTCTCAACAGAGTGGCAGCTGGCGCTCACACGTTTCGGAGGG	300	
DB	241	GAAGATATCCAGATTATTACTCTCAACAAAGTGATAGCTGGCCACCACGTTTCGGAGGG	300	
QY	301	GGGACCAAGCTGGAAATTAA	320	
DB	301	GGGACCAAGCTGGAGATAAA	320	

RESULT 12
 US-08-485-246A-3
 ; Sequence 3, Application US/08485246A
 ; Patent No. 6072035
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardman, No. 6072035man
 ; APPLICANT: Kolbinger, Frank
 ; APPLICANT: Saidanha, Jose
 ; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
 ; TITLE OF INVENTION: Immunoglobulin isotype
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6072035artis Patent Department
 ; STREET: 59 Route 10
 ; CITY: East Hanover

|||||

Db 301 GGGACCAAGCTGGAGAT 317

RESULT 15

US-08-800-198-3

: Sequence 3, Application US/08800198

: Patent No. 5942602

: GENERAL INFORMATION:

: APPLICANT: WELS, WINFRIED S.

: APPLICANT: SCHMIDT, MATTHIAS

: APPLICANT: VAKALOPOULOU, EVANGELIA

: APPLICANT: SCHNEIDER, DOUGLAS

: TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES

: NUMBER OF SEQUENCES: 17

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.

: STREET: 2200 CLARENDON BLVD. SUITE 1400

: CITY: ARLINGTON

: STATE: VA

: COUNTRY: US

: ZIP: 22201

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/800,198

: FILING DATE: 13-FEB-1997

: CLASSIFICATION: 530

: ATTORNEY/AGENT INFORMATION:

: NAME: HAMLET-KING, DIANA

: REGISTRATION NUMBER: 33,302

: REFERENCE/DOCKET NUMBER: SCH 1576

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 703-243-6333

: TELEFAX: 703-243-6410

: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 318 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: linear

: MOLECULE TYPE: other nucleic acid

: HYPOTHETICAL: NO

: ANTI-SENSE: NO

US-08-800-198-3

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US-08-800-198-3

Query Match      68.2%; Score 218.8; DB 2; Length 318;
Best Local Similarity 80.5%; Pred. No. 9.4e-64;
Matches 256; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY    1   GATATTGTGCTAAACTCAGTCTCCAGCCACCCTGCTGTGCACACCAGGAGATAGCGTCAGT 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    1   GACATCCAGCTGACCCAGTCTCCAGCCATCTGTGTGAGTCCAGGAGAAGAAGTCAGT 60

QY    61  CTTTCTGCCAGGCGAGCCAAAGTATTAGCAACCACTTACACTGGTATCAACAATAATCA 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    61  TTCTCCTCGAGGGCGAGTCAGAGCATTTGGCACAAATATACACTGGTATCAGCAAAGAACA 120

QY    121 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCAATCTCTGGGATCCCCTCC 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    121 AATGGTCTTCCAAGGCTTCTCATAAAGTATGCTTCTTGAGTATATCTCTGGGATCCCCTTCC 180

QY    181 AGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCGGTCTTCAGTATCAACAGTGTGGAGACT 240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    181 AGGTTTAGTGGCATGGATCAGGACAGATTTTTACTCTTAGCNTCAACAGTGTGGAGTCT 240

QY    241 GAAGATTTTGAATGTAATTTCTGTCAACAGAGTGGCAGCTGGCCTTCACACGTTTCGGAGG 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB    241 GCAGATATTGCAGATTAATTACTGTCAACAAGTGTATAGCTGGCAACCAACGCTTCGGTGCT 300

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Qy 301 GGGACCAAGCTGGAATT 318
||||| ||||| || |||
Db 301 GGGACCAAGCTCGAGATT 318

Search completed: October 11, 2001, 15:14:15
Job time: 5002 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:32 ; Search time 2122.65 Seconds
(without alignments)
2339.127 Million cell updates/sec

Title: US-08-791-391A-31
Perfect score: 321
Sequence: 1 GAGATTGCTAACTCAGTC.....GGACCAAGTGGAATTAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: gb_ba2:*
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- 94: gb_rol:*
- 95: gb_rol2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	318.6	99.3	321	9	AX060782 Sequence
2	318	99.1	321	9	AX060810 Sequence
3	265.8	82.8	321	9	AX060786 Sequence
4	247.2	77.0	321	94	MUSCMVF Mouse mRNA
5	247.2	77.0	321	94	MUSIGRACY Mouse lysoz
6	247.2	77.0	370	94	MUSIGRDX Mouse Ig ac
7	245.6	76.5	321	94	AF163757 Mus muscu
8	245.6	76.5	321	94	MUSCMVF Mouse mRNA

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9 245.6 76.5 381 10 E07933
10 245.6 76.5 381 10 I31959
11 245.6 76.5 381 10 I78571
12 245.6 76.5 381 10 I78626
13 245.6 76.5 431 94 M05162
14 244.4 76.1 324 94 AF139844
15 244 76.0 324 94 AF139849
16 244 76.0 330 94 M05162
17 244 76.0 330 94 M05162
18 242.4 75.5 324 94 AB048528
19 242.4 75.5 324 94 AF139845
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26 240.8 75.0 321 94 M05162
27 240.8 75.0 324 94 AF139847
28 240.8 75.0 324 94 AF139848
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30 240.4 74.9 324 94 M05162
31 239.6 74.6 420 94 M05162
32 239.6 74.6 5238 94 A07699
33 239.2 74.5 324 94 AF087031
34 238.6 74.3 317 94 M05162
35 238 74.1 317 94 M05162
36 235 73.2 313 94 M05162
37 234.6 73.1 321 94 M05162
38 234.4 73.0 381 94 M05162
39 234.2 73.0 307 94 M05162
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41 233.8 72.8 318 94 M05162
42 233.6 72.8 323 94 M05162
43 233.2 72.6 306 94 M05162
44 233.2 72.6 315 94 M05162
45 232.8 72.5 300 94 M05162
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ALIGNMENTS

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RESULT 1
AX060782 AX060782 321 bp DNA PAT 22-JAN-2001
LOCUS Sequence 3 from Patent WO0078815.
DEFINITION
ACCESSION AX060782
VERSION AX060782.1 GI:12406162
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
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BASE COUNT 78 a 93 c 79 g 71 t
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Best Local Similarity 99.1%; Pred. No. 3.4e-86;
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QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGCGCT 60
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QY 121 GGTCAAGCCCAAGGCTTCATCCKKTTATAGCAACACCTACACTGGTATCAACAAGGCCT 180
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LOCUS Sequence 31 from Patent WO0078815.
DEFINITION
ACCESSION AX060810
VERSION AX060810.1 GI:12406189
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 31 28-DEC-2000;
Applied Molecular Evolution (US)
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/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="grafted antibody variable region"
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variation
BASE COUNT 76 a 93 c 78 g 71 t 3 others
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QY 121 GGTCAAGCCCAAGGCTTCATCCKKTTATAGCAACACCTACACTGGTATCAACAAGGCCT 180
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LOCUS AX060786 321 bp DNA PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent W00078815.
ACCESSION AX060786
VERSION AX060786.1 GI:12406166
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2,g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 7 28-DEC-2000;
APPLIED Molecular Evolution (US)
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Best Local Similarity 88.8%; Pred. No. 3.9e-70;
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Best Local Similarity 85.3%; Pred. No. 1.8e-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

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RESULT 5
LOCUS MUSIGKACY 321 bp mRNA ROD 27-APR-1993
DEFINITION Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
mRNA, partial cds.
ACCESSION M35667
VERSION M35667.1 GI:196584
KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; processed gene;
variable region VK23.
SOURCE Mouse hybridoma, cDNA to mRNA, clone 10K-106.
ORGANISM Mus musculus

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LOCUS MUSCMVF 321 bp mRNA ROD 26-JUL-1993
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95943
VERSION M95943.1 GI:309175
KEYWORDS
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Simpson,J.A., Chow,J.C., Baker,J., Avdaloovic,N.M., Yuan,S.,
Co.M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
TITLE Untitled
JOURNAL Unpublished (1992)
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Best Local Similarity 85.3%; Pred. No. 1.8e-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

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RESULT 5
LOCUS MUSIGKACY 321 bp mRNA ROD 27-APR-1993
DEFINITION Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
mRNA, partial cds.
ACCESSION M35667
VERSION M35667.1 GI:196584
KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; processed gene;
variable region VK23.
SOURCE Mouse hybridoma, cDNA to mRNA, clone 10K-106.
ORGANISM Mus musculus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and Brooks, W.B.R.
TITLE A three-dimensional model of an anti-lysozyme antibody
JOURNAL J. Mol. Biol. 194, 713-724 (1987)
MEDLINE 88011212
FEATURES Location/Qualifiers
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RESULT 6
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LOCUS Mouse Ig active kappa-chain V-region, partial cds.
DEFINITION M93959
ACCESSION M93959
VERSION M93959.1 GI:197572
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 370)
AUTHORS Takeda, I., Wise, K.S. and Hoffman, R.W.
TITLE Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a monoclonal antibody specific for a unique set of small nuclear ribonucleoprotein complexes
JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)
MEDLINE 92575706
FEATURES Location/Qualifiers

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BASE COUNT 96 a 90 c 86 g 98 t
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Best Local Similarity 85.3%; Pred. No. 1.8e-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;
QY 1 GAGATTGCTGCTACTAGTCTCCAGCCACCCTGTCTCTCAGCCGAGGAGGCGACT 60
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RESULT 7
AF163757 AF163757 321 bp mRNA ROD 04-AUG-1999
LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.
ACCESSION AF163757
VERSION AF163757.1 GI:5690320
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal Mouse Monoclonal Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 321)
AUTHORS Mertens, N.M. and Cunningham, M.W.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma University Health Sciences Center, 940 St. Young Blvd, Oklahoma

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Matches 272;	Conservative 2;	Mismatches 46;	Indels 0;	Gaps 0;
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QY	61	CTTTCTGCGCAGGCGCAGCAAAAGTATTAGCAACACCCTACACTGGTATATCAACAAGGCCT	120	
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QY	301	GGGACCAAGTGGAAATTA 320		
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ACCESSION	E07933			
VERSION	E07933.1 GI:2176065			
KEYWORDS	JP 1994217786-A/2.			
SOURCE	Mus sp. .			
ORGANISM	Mus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y. .			
JOURNAL	ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT			
COMMENT	ENCODING THE SAME ANTIBODY			
	Patent: JP 1994217786-A 2 09-AUG-1994;			
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	PN JP 1994217786-A/2			
	PD 09-AUG-1994			
	PF 28-NOV-1992 JP 1992341255			
	PI KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI			
	TOKIYOSHI YUKIO			
	PC C12P21/08.A61K39/395,C07K15/00,C12N15/13,(C12P21/08,C12R1:91);			
	CC strandedness: Double;			
	CC topology: Linear;			
	CC hypothetical: No;			
	CC anti-sense: No;			
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ACCESSION AF139849
VERSION AF139849.1 GI:4732162
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
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location/Qualifiers
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BASE COUNT 87 a 82 c 74 g 81 t
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Best Local Similarity 84.7%; Pred. No. 1.7e-63;
Matches 271; Conservative 2; Mismatches 47; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGCTCTCTCAGCCAGGAGAAAGGGGCACT 60
DB 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGCTCTCTCAGTCCAGGAGATAGCGTCAGT 60
QY 61 CTTTCTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCCT 120
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QY 121 GGTCACAGCCCAAGGCTTCTCATCMKKTATCTGTTCCAGTCCATCTCTGGGATCCCGCC 180
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Search completed: October 11, 2001, 15:09:33
Job time: 6355 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:34:05 ; Search time 2341.88 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 20456230

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	217.2	67.7	738	150	BF582153 602099743
2	211.6	65.9	949	150	BF579007 602096124
3	206	64.2	946	155	BG569760 602590367
4	205.6	64.0	434	115	AW406486 UI-HF-BL0
5	204.4	63.7	398	115	AW405309 UI-HF-BL0
6	202.8	63.2	482	32	AV733856 AV733856
7	201.2	62.7	519	115	AW405183 UI-HF-BL0
8	200.8	62.6	385	115	AW405025 UI-HF-BL0
9	199.6	62.2	468	115	AW405643 UI-HF-BL0
10	199.2	62.1	624	166	BE306691 601104076
11	198	61.7	468	115	AW404506 UI-HF-BL0
12	198	61.7	1015	155	BG536848 602566386
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14	195.4	60.9	548	155	BG568486 602587455
15	194.8	60.7	485	110	AV734882 AV734882
16	193	60.1	451	170	BF74574 IL3-ET011
17	193	60.1	758	154	BG534598 602553450
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19	191.6	59.7	514	115	AW405207 UI-HF-BL0
20	191.6	59.7	615	122	AW959456 EST371526
21	191.4	59.6	461	115	AW406219 UI-HF-BL0
22	191.4	59.6	849	150	BF583521 602101553
23	191.4	59.6	1061	151	BF663663 602143371
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25	189.2	58.9	656	154	BG482934 602502942
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27	187.6	58.4	639	32	AV734416 AV734416
28	186.8	58.2	443	115	AW405460 UI-HF-BL0
29	186.8	58.2	448	115	AW404726 UI-HF-BL0
30	185.8	57.9	868	155	BG539952 602567464
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32	185.4	57.8	317	115	AW404261 UI-HF-BL0
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37	181.8	56.6	518	115	AW406576 UI-HF-BL0
38	181.8	56.6	644	115	AW405817 UI-HF-BL0
39	181.6	56.6	719	154	BG536027 602564303
40	181.6	56.6	895	151	BF663197 602144313
41	181.2	56.4	473	115	AW406934 UI-HF-BL0
42	180.8	56.3	1047	155	BG545546 602572793
43	180.4	56.2	425	115	AW406785 UI-HF-BL0
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ALIGNMENTS

RESULT	1	2
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DEFINITION	602099743F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4219402 5', mRNA sequence.	602096124F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4216180 5', mRNA sequence.
ACCESSION	BF582153	BF579007
VERSION	BF582153.1	BF579007.1
KEYWORDS	EST.	EST.
SOURCE	house mouse.	house mouse.
ORGANISM	Mus musculus	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 738)	1 (bases 1 to 949)
TITLE	NIH-MGC http://mgc.nci.nih.gov/	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov	Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9801 row: f column: 11

High quality sequence stop: 714.

Location/Qualifiers

FEATURES

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1. .738

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/clone_lib="NCI_CGAP_Co24"

/lab_host="DH10B (TI phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

210 a 189 c 172 g 167 t

BASE COUNT

ORIGIN

Query Match 67.7%; Score 217.2; DB 150; Length 738;

Best Local Similarity 84.0%; Pred. No. 3.3e-56;

Matches 267; Conservative 2; Mismatches 45; Indels 4; Gaps 2;

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Db 78 TGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCTCAGTCTTTC 137

QY 66 CTGCCAGGCGAGCCAAAGATTAGCAACCACTAGACTGGTATCACAAAGCGCTGGTCA 125

Db 138 CTGCCAGGCGAGCCAAAGATTAGCAACCACTAGACTGGTATCACAAAGCGCTGGTCA 197

QY 126 AGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCCAGGTT 185

Db 198 GTCTCCAAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCCAGGTT 257

QY 186 CAGTGGCAGTGGATCAGGACAGATTTCACCCCTACTATCTCCAGTCTGGAGCGCTGAAGA 245

Db 258 CAGTGGCAGTGGATCAGGACAGATTTCACCTCTCAGTATCACACAGTGTGGAGACTGAAGA 317

QY 246 TTTTGCAGTCTATTACTGTCTACACAGAGTGGCAGCTGGCCTCA---CACGTTGGAGGGG 302

Db 318 -TTTGGAGTATTTCTGTCAACAGAGTAACAGCTGGCCTCAGCTCAGCTCGGTGCTGG 376

QY 303 GACCAAGGTGGAAATTAA 320

Db 377 GACCAAGCTGGAGCTGAA 394

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9792 row: p column: 05
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
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ORIGIN

Query Match 65.9%; Score 211.6; DB 150; Length 949;
Best Local Similarity 81.2%; Pred. No. 1.9e-54;
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DB 83 TGTACTACTCAGTCTCCAGCCAGCCCTGTCTGTGACTCCAGGAGATAGCGTCACTCTTC 142
QY 66 CTGCAGCCAGGCAAAAGTATTAGCAACCCTACACTGGTATCAACAAAGGCGTGTCA 125
DB 143 CTGAGGCCAGCAAAAGTATTAGCAACACCTACACTGGTATCAACAAATCACATGA 202
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QY 306 CAAGGTGGAAATTA 319
DB 382 CAAACTGGAGCTGA 395

RESULT 3

BG569760
LOCUS 602590367F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717049 5', mRNA sequence.
DEFINITION BG569760
ACCESSION BG569760.1 GI:13577413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 946)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CMI566 row: e column: 18
High quality sequence stop: 738.

FEATURES

source
1. .946
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4717049"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGGCACATG-dn(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 295 a 248 c 247 g 156 t
ORIGIN

Query Match 64.2%; Score 206; DB 155; Length 946;
Best Local Similarity 77.5%; Pred. No. 1e-52;
Matches 248; Conservative 1; Mismatches 71; Indels 0; Gaps 0;
QY 1 GAGATTGTCTAAGTCTCAGCCAGCCCTGTCTCAGCCAGGAGAAAGGGGAGCT 60
DB 96 GAATTCGTGTGACACAGTCTCCAGCCACCTCTCTTTGTCTCCAGGGGAAGGACACC 155
QY 61 CTTTCTCCAGGCGCCAGCAAAAGTATTAGCAACACCTACACTGTGTATCAACAAAGGCT 120
DB 156 CTCCTCTCGAGGGCGAGAGTGTAGCAGCCACTTAGCCTGTGTACCAACAGAACT 215
QY 121 GGTCAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCAGTCCATCTCTGGATCCCGCC 180
DB 216 GGCCAGGCTCCAGGCTCCCTCATCTATGATGCATCCACAGGGCCACTGGCATCGCAGCC 275
QY 181 AGGTTTCAAGTGGCAGTGGATCAGGACAGATTTTCACTCATCTCCAGTCTCCAGTCTGGAGCT 240
DB 276 AGGTTTCAAGTGGCAGTGGGTCGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCT 335
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTGGCTCAGCTCGGAGGG 300
DB 336 GAAGATTTTGCAGTTTATTACTGTGACAGGCTAGCAACTGGGCGCTCAGTTTCGGCGGA 395
QY 301 GGGACCAAGGTGGAAATTA 320
DB 396 GGGACCAAGGTGGAGATTA 415

RESULT 4

AW406486
LOCUS UI-HF-BLO-acr-f-12-0-UI.F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060238 5', mRNA sequence.
DEFINITION AW406486
ACCESSION AW406486.1 GI:6925543
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

REFERENCE 1 (bases 1 to 385)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
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 1..385
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3058252"
 /clone_lib="NIH_MGC_37"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LT1)"
 /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Ronaldo, Ph.D. and M. Bento Soares, Ph.D." 85 t

BASE COUNT 88 a 114 c 98 g 85 t
 ORIGIN
 Query Match 62.6%; Score 200.8; DB 115; Length 385;
 Best Local Similarity 76.7%; Pred. No. 3e-51;
 Matches 244; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

QY 3 GATTGTCTTAACCTCAGCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACTCT 62
 DB 7 GATTGTCTTACAGAGCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACTCT 66
 QY 63 TTCTGTCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCTGG 122
 DB 67 CTCCTGCGAGGCCAGTCCAGAGTGTTCGAGCTACTTAGCCTGGTATCCACAGAAACCTGG 126
 QY 123 TCAGCCCGAGGCTCTCATCMKKTATCGTCCAGTCCCATCTCTGGATCCCGCCAG 182
 DB 127 CCAGGCTCCAGGCTCTCATCTATGATGATCCACAGGGCCACTGGCATCCCGCCAG 186
 QY 183 GTTCAGTGGCAGTGGATCAGGAGCAGATTTACCCCTCACATCTCTCCAGTCTGGAGCCTGA 242
 DB 187 GTTCAGTGGCAGTGGGCTCGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGA 246
 QY 243 AGATTTGCACTATTACTGTCAACAGATGGCAGCTGGCCTCACAGTTCGAGGGGG 302
 DB 247 AGATTTGCACTATTACTGTCAACAGATGGCAGCTGGCCTCACAGTTCGAGGGGG 306
 QY 303 GACCAAGGTGGAATTA 320
 DB 307 GACGAAGGTGGAATTA 324

RESULT 9
 AW405643
 LOCUS AW405643 468 bp mRNA EST 16-FEB-2000
 DEFINITION UI-HF-BL0-abs-F-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3057561 5', mRNA sequence.
 ACCESSION AW405643
 VERSION AW405643.1 GI:6924700
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 468)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
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 1..468
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057561"
 /clone_lib="NIH_MGC_37"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LT1)"
 /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Ronaldo, Ph.D. and M. Bento Soares, Ph.D." 106 t

BASE COUNT 110 a 137 c 115 g 106 t
 ORIGIN
 Query Match 62.2%; Score 199.6; DB 115; Length 468;
 Best Local Similarity 76.2%; Pred. No. 7.6e-51;
 Matches 244; Conservative 1; Mismatches 75; Indels 0; Gaps 0;

QY 1 GAGATTGTCTTAACCTCAGCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACT 60
 DB 23 GAAATTGTGTGACAGAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACT 82
 QY 61 CTTTCTCTGCCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
 DB 83 CTCCTCTCGAGGGCCAGTCCAGAGTGTAGCGCTACTTAGCCTGGTATCCACAGAAACCT 142
 QY 121 GGTCAAGCCCCAAGGCTCTCATCMKKTATCGTCCAGTCCCATCTCTGGATCCCGCC 180
 DB 143 GGCCAGGCTCCAGGCTCCCTCATCTATGATGATCCCAACAGGGCCACTGGCATCCCGCC 202
 QY 181 AGGTTCAAGTGGCAGTGGATCAGGAGCAGATTTACCCCTCACATCTCTCCAGTCTGGAGCCT 240
 DB 203 AGGTTCAAGTGGCAGTGGTCTGGGACAGAGTCTCACTCTCACCATCAGCAGCCTAGAGCCT 262
 QY 241 GAAGATTTGCACTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGAGGG 300
 DB 263 GAAGATTTGCACTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGAGGG 322
 QY 301 GGGACCAAGGTGGAATTA 320
 DB 323 GGGACCAAGGTGGAATTA 342

RESULT 10
 BE306691
 LOCUS BE306691 624 bp mRNA EST 26-OCT-2000
 DEFINITION 601104076f1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3501355 5',
 mRNA sequence.
 ACCESSION BE306691
 VERSION BE306691.1 GI:9160297
 KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 624)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8561 row: 9 column: 20
High quality sequence stop: 598.

FEATURES
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Location/Qualifiers
1..624
/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db_xref="taxon:10090"
/clone_lib="IMAGE:3501355"
/tissue_type="spontaneous tumor, metastatic to mammary."
/lab_host="DH10B"
/note="Organ: Lung; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 172 a 166 c 145 g 141 t
ORIGIN

Query Match
Best Local Similarity 62.1%; Score 199.2; DB 166; Length 624;
Matches 243; Conservative 2; Mismatches 75; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
DB 59 GACATCTGTATGACCCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 119 CTTTCCTGTAGGGCCAGCCAGATATTACAGAAACCTACACTGGTATCAACAAGGCGCT 120
QY 121 GGTCACAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCAGTCCATCTCTGGGATCCCGCC 180
DB 179 CATGGGACTCCAAGGCTTCTCATCAAGTATGACCTGATCCCATCTCTGGGATCCCGCC 238
QY 181 AGGTTTCAGTGGCAGTGATCAGGAGAGATTTACCTCCTCACTCTCCAGTCTGGAGCGCT 240
DB 239 AGGTTTCAGTGGCAGTGATCAGGAGAGATTTACCTCCTCACTCTCCAGTCTGGAGCGCT 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTTCCAGTCTGGAGCGCT 298
DB 299 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTTCCAGTCTGGAGCGCT 300
QY 301 GGGACCAAGGTTGGAATTA 320
DB 359 GGGACCAAGGTTGGAATTA 378

RESULT 11
AW404506 468 bp mRNA
LOCUS
DEFINITION UT-HF-BL0-aby-a-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058065 5', mRNA sequence.
ACCESSION AW404506
VERSION AW404506.1 GI:6923563

KEYWORDS SOURCE EST.
ORGANISM human.
Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058065"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LT1)"
/note="Vector: pT7-Tac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 106 a 137 c 114 g 111 t
ORIGIN

Query Match
Best Local Similarity 61.7%; Score 198; DB 115; Length 468;
Matches 243; Conservative 1; Mismatches 76; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
DB 41 GAAATTTGTGACACAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
DB 101 CTCTCTGTCAGGCGCAGTCTAGAGTGTGACGCTTACCTTACCTTACCTTACCTTACCT 160
QY 121 GGTCACAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCAGTCCATCTCTGGGATCCCGCC 180
DB 161 GGCAGGCTCCAGGCTCTCTATGATGATCATCAACAGGCGCTTCCAGCTCCAGCT 230
QY 181 AGGTTTCAGTGGCAGTGATCAGGAGAGATTTACCTCCTCACTCTCCAGTCTGGAGCGCT 240
DB 221 AGGTTTCAGTGGCAGTGATCAGGAGAGATTTACCTCCTCACTCTCCAGTCTGGAGCGCT 280
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTTCCAGTCTGGAGCGCT 300
DB 281 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTTCCAGTCTGGAGCGCT 300
QY 301 GGGACCAAGGTTGGAATTA 320
DB 341 GGGACCAAGGTTGGAATTA 360

RESULT 12
BG536848 1015 bp mRNA
LOCUS
DEFINITION BG536848 1015 bp mRNA
IMAGE:602566386F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691085 5',
mRNA sequence.

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ACCESSION      BG536848
VERSION        BG536848.1  GI:13528394
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1CM1509 row: k column: 22
              High quality sequence stop: 624.
              Location/Qualifiers
                1..1015
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4691085"
                /lab_lib="NIH_MGC_77"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1;
                SfiI (ggcgctggccc); Site:2: SfiI (ggccattggccc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGCCATTATGCG-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.9
                kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC Library."
              BASE COUNT  273 a 284 c 251 g 205 t
              ORIGIN
              Query Match      61.7%; Score 198; DB 155; Length 1015;
              Best Local Similarity 75.9%; Pred. No. 3e-50;
              Matches 243; Conservative 1; Mismatches 76; Indels 0; Gaps 0;

QY  1  GAGATTGTGCTAACTAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGAGAGGCGGCT 60
Db  95  GAAATTGTGTGACACAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGAGAGGCGGCT 154
QY  61  CTTTCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 120
Db  155  CTCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 214
QY  121  GGTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db  215  GGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 274
QY  181  AGGTTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
Db  275  AGGTTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 334
QY  241  GAAGATTTCGAGTCTATTACTGTCAACAGAGTGGCGGCGGCGGCGGCGGCGGCGG 300
Db  335  GAAGATTTCGAGTCTATTACTGTCAACAGAGTGGCGGCGGCGGCGGCGGCGGCGG 394
QY  301  GGGACCAAGTGGGAAATTA 320
Db  395  GGGACCAAGTGGGATCA 414

FEATURES      source
              Location/Qualifiers
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                /clone="IMAGE:3058518"
                /clone_lib="NIH_MGC_37"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LT1)"
                /note="Vector: pT73-Pac; Site:1: NotI; Site:2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
              BASE COUNT  108 a 139 c 115 g 103 t
              ORIGIN
              Query Match      61.2%; Score 196.4; DB 115; Length 465;
              Best Local Similarity 75.6%; Pred. No. 7.4e-50;
              Matches 242; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

QY  1  GAGATTGTGCTAACTAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGAGAGGCGGCT 60
Db  85  GAAATTGTGTGACACAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGAGAGGCGGCT 144
QY  61  CTTTCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 120
Db  145  CTCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 204
QY  121  GGTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db  205  GGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 264
QY  181  AGGTTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
Db  265  AGGTTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 324
QY  241  GAAGATTTCGAGTCTATTACTGTCAACAGAGTGGCGGCGGCGGCGGCGGCGGCGG 300
Db  325  GAAGATTTCGAGTCTATTACTGTCAACAGAGTGGCGGCGGCGGCGGCGGCGGCGG 384
QY  301  GGGACCAAGTGGGAAATTA 320
Db  385  GGGACCAAGTGGGATCA 404

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RESULT 14
BG568486      548 bp      mRNA      EST      10-APR-2001
LOCUS         602587455F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4716468 5',
DEFINITION    mRNA sequence.
ACCESSION     BG568486
VERSION       BG568486
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       1 (bases 1 to 548)
TITLE         NIH-MGC http://mgc.nci.nih.gov/
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cnapbs-r@mail.nih.gov
              Tissue Procurement: CLONETECH Laboratories, Inc.
              cDNA Library Preparation: CLONETECH Laboratories, Inc.
              DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              Cloning by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1564 row: m column: 13
              High quality sequence stop: 548.
FEATURES     Location/Qualifiers
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              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:4716468"
              /lab_host="NIH_MGC_76"
              /lab_host="DH10B (T1 phage-resistant)"
              /note="organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
              SfiI (ggccgctggcc); Site_2: SfiI (ggccattatggcc); 5' and
              3' adaptors were used in cloning as follows: 5' adaptor
              sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:
              5'-ATTCTAGAGCGGCGGCGGAGATG-dt(30)BN-3' (where B = A,
              C, or G and N = A, C, G, or T). Average insert size 1.85
              kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
              by PCR. This library was enriched for full-length inserts
              and was constructed by Clontech Laboratories (Palo Alto,
              CA). Note: this is a NIH_MGC Library."
BASE COUNT   126 a 162 c 139 g 121 t
ORIGIN

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QY 301 GGGACCAAGGTGGAAATTA 319
Db 406 GGGACCAAGGTGGAAATCA 424

RESULT 15
LOCUS         AV734882
DEFINITION    AV734882 cda Homo sapiens cDNA clone cdABFC04 5', mRNA sequence.
ACCESSION     AV734882
VERSION       AV734882.1 GI:10852427
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       1 (bases 1 to 485)
TITLE         Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
              Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
              W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J.,
              Chen, Z. and Han, Z.
              Homo sapiens cDNA cda clones
              Unpublished (2000)
              Contact: Zequang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex.45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.
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ORIGIN

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Query Match      60.9%; Score 195.4; DB 155; Length 548;
Best Local Similarity 75.3%; Pred. No. 1.6e-49;
Matches 241; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

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Db 106 GAAATTGTGTGACAGTCTCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

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Db 166 CTCCTCGAGGCGGAGTTCAGATGTTGGAGCTACTTACCTGGTATCAACAAAGGCT 120

QY 121 GGTCAAGCCCAAGGCTCTCATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGCC 180
Db 226 GGCAGGCTCCAGGCTCTCATCTATGATAGTCCAAAGGCGGCACTGGCTCCAGCC 285

QY 181 AGTTTCAGTGGAGTGGATCAGGAGACAGTTCACCTCCTACTATCTCCAGTCTGGAGCT 240
Db 286 AGTTTCAGTGGAGTGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCT 345

QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACCTTTCGGAGG 300
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Query Match      60.7%; Score 194.8; DB 110; Length 485;
Best Local Similarity 75.3%; Pred. No. 2.3e-49;
Matches 241; Conservative 1; Mismatches 78; Indels 0; Gaps 0;

QY 1 GAGATTGCTAAGTCTCAGTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
Db 92 GAAATTGTGTGACAGTCTCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT 151

QY 61 CTTCCTCGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCT 120
Db 152 CTTCCTCGAGGCGGAGTTCAGATGTTGGAGCTACTTACCTGGTATCAACAAAGGCT 211

QY 121 GGTCAAGCCCAAGGCTCTCATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGCC 180
Db 212 GGCAGGCTCCAGGCTCTCATCTCTGATGATCATCAACAGGCGGCTGGCATCCACCC 271

QY 181 AGTTTCAGTGGAGTGGATCAGGAGACAGTTCACCTCCTACTATCTCCAGTCTGGAGCT 240
Db 272 AGTTTCAGTGGAGTGGTCTGGGACAGCTTCACTCTCACCATTACAGCTTAAGCT 331

QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACCTTTCGGAGG 300
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QY 301 GGGACCAAGGTGGAAATTA 320
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Thu Oct 11 16:16:08 2001

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Job time: 5542 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:39 ; Search time 177.65 seconds
(without alignments)
1134.570 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	319.8	99.6	321	19 AAV49843	LM609 antibody lig
2	318.6	99.3	321	19 AAV49821	Vitaxin antibody l
3	318.6	99.3	321	22 AAF28176	Vitaxin light chal
4	318	99.1	321	22 AAF28199	DNA encoding light
5	265.8	82.8	321	19 AAV49823	LM609 antibody lig
6	265.8	82.8	321	22 AAF28178	Antibody LM609 lig
7	258.4	80.5	381	21 AA235244	Humanised anti-ver
8	250.4	78.0	321	20 AAV71800	Humanised anti-alp
9	250.4	78.0	338	20 AAV71802	Vitronectin alpha-
10	245.6	76.5	381	15 AAQ64167	Sequence of mouse
11	245.6	76.5	381	22 AAF58747	Murine CMV5 antibo

12	239.6	74.6	5238	11 AAQ4654	Plasmid pBR111 enc
13	239.2	74.5	324	20 AAV71798	Murine vitronectin
14	232.8	72.5	381	21 AA235242	Mouse anti-verotox
15	231.6	72.1	651	21 AAA44346	Human secreted exp
16	229.6	71.5	416	18 AAT49345	CDNA encoding kapp
17	228.4	71.2	415	21 AAD0904	Humanised antibody
18	228.4	71.2	415	21 AAD0906	Humanised antibody
19	228	71.0	324	17 AAT33446	EGF receptor chime
20	223.6	69.7	486	14 AAQ43245	hIL2R Ab L chain V
21	223.6	69.7	8858	20 AA210202	Expression vector
22	222	69.2	363	17 AAT38510	Light chain coding
23	218.8	68.2	415	21 AAD01262	Mouse monoclonal a
24	216.6	67.5	315	20 AAV71803	Jk gene segment.
25	216.6	67.5	315	20 AAV71805	Humanised anti-alp
26	214	66.7	321	20 AA210203	DNA encoding the v
27	213.6	66.5	322	15 AAQ44714	Light chain variab
28	213.6	66.5	322	20 AA228545	DNA encoding the v
29	209.2	65.2	321	20 AA210205	Human Fab clone LP
30	206	64.2	324	22 AAF29505	Anti-IL2R-beta ant
31	205.6	64.0	322	14 AAQ36615	Insert coding for
32	205.6	64.0	1395	10 AAN90300	B-B10 MAB L chain
33	204	63.6	321	14 AAQ43243	Anti-gp54 MAB 48-1
34	204	63.6	321	19 AAV26766	L-chain V-region o
35	204	63.6	486	14 AAQ43384	Anti-human TNF-alp
36	202.8	63.2	642	20 AAX77408	H. pylori beta-ure
37	202.4	63.1	321	21 AAA40203	CDNA encoding kapp
38	202.4	63.1	381	18 AAT49338	CDNA encoding kapp
39	202.4	63.1	416	18 AAT49344	CDNA encoding kapp
40	202.4	63.1	416	18 AAT49342	CDNA encoding kapp
41	201	62.6	318	14 AAQ48766	Monoclonal antibod
42	200.8	62.6	381	19 AAV12262	Monoclonal antibod
43	199.8	62.2	720	19 AAV26770	Anti-gp54 MAB 48-1
44	199.2	62.1	794	17 AAT42033	Plasmid pMW152-225
45	199.2	62.1	2070	17 AAT42035	Plasmid pSW202-225

ALIGNMENTS

RESULT 1
AAV49843
ID AAV49843 standard; DNA; 321 BP.

XX AAV49843;

XX 02-NOV-1998 (first entry)

XX LM609 antibody light chain variable region DNA grafted fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT CDS 1..321

FT /*tag= a

FT /product= "LM609 grafted antibody light chain variable

FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

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XX  Glaser SM, Huse WD;
XX  WPI: 1998-437472/37.
XX  P-PSDB; AAW76006.
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX  integrin - and related grafted antibodies based on murine monoclonal
XX  LM609, also related nucleic acid, used to treat, prevent or diagnose
XX  angiogenesis or restenosis
XX  Claim 24; Fig 7; 129pp; English.
XX  This sequence encodes a LM609 grafted antibody variable light chain
XX  region. LM609 and the antibody vitaxin bind selectively to integrin
XX  alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
XX  and thus block integrin-mediated signal transduction. This is useful in
XX  the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
XX  specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX  etc.). The antibodies contain non-murine framework regions so are
XX  suitable for use in humans. Enhanced types of LM609 have affinity more
XX  than 90 times greater than that of parent the parent antibody.
XX  Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
SQ

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OS  Mus sp.
XX  Key
XX  CDS
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XX  /product= "vitaxin antibody light chain variable region"
XX  /note= "partial sequence, no start or stop codon given"
XX  WO9833919-A2.
XX  06-AUG-1998.
XX  30-JAN-1998; 98WO-US01826.
XX  30-JAN-1997; 97US-0791391.
XX  (IXSY-) IXSYS INC.
XX  Glaser SM, Huse WD;
XX  WPI: 1998-437472/37.
XX  P-PSDB; AAW76002.
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX  integrin - and related grafted antibodies based on murine monoclonal
XX  LM609, also related nucleic acid, used to treat, prevent or diagnose
XX  angiogenesis or restenosis
XX  Claim 6; Fig 1b; 129pp; English.
XX  This sequence encodes the vitaxin antibody variable light chain region.
XX  Vitaxin and the antibody LM609 bind selectively to integrin alphaVbeta3
XX  and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
XX  block integrin-mediated signal transduction. This is useful in the
XX  treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
XX  specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX  etc.). The antibodies contain non-murine framework regions so are
XX  suitable for use in humans. Enhanced types of LM609 have affinity more
XX  than 90 times greater than that of parent the parent antibody.
XX  Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ

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Query Match      99.3%; Score 318.6; DB 19; Length 321;
Best Local Similarity 99.1%; Pred. No. 6.9e-91;
Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db  61 ctctctgccagggccagcaagattatagcaaccacctacactgtgtatcaacaaggcct 120

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ID  AAV49821
XX  AAV49821 standard; DNA; 321 BP.
XX  AAV49821;
XX  02-NOV-1998 (first entry)
XX  Vitaxin antibody light chain variable region DNA.
XX  Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX  LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX  diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX  neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX  macular degeneration; osteoporosis; ss.

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Db 121 ggtcaagccccaggcttctctatcnnmtatgttcccaagtcacatctctggtggtcccccgc 180

Qy 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACCCCTCAGTTCATCTCCAGTGTGAGCCT 240
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Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG 300
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Qy 301 GGGACCAAGGTGGAATTAAG 321
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Db 301 gggaccaaggtggaattaa 321
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RESULT 5
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ID AAV49823 standard; DNA; 321 BP.
XX
AC AAV49823;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 antibody light chain variable region DNA fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT FT /*tag= a
FT FT /product= "LM609 antibody light chain variable region"
FT FT /note= "partial sequence, no start or stop codon given"
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
WPI; 1998-437472/37.
DR P-PSDB; AAW75004.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 40; Fig 2b; 129pp; English.
XX
XX This sequence encodes the LM609 antibody variable light chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX

SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 82.8%; Score 265.8; DB 19; Length 321;
Best Local Similarity 88.8%; Pred. No. 2.9e-74;
Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;

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Db 1 gatattgttaactcagtcagtcagccacctgtctgtgacaccagagatagcgtcag 60
|||||

Qy 61 CTTTCCTGCCAGGCGAGCCAAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCGCT 120
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Db 61 ctttctgcccagggccagccaaagtatttagcaaccacctacactgttatcaacaaatca 120
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Qy 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATGTTTCCAGTCCATCTCTGGGATCCCCGCC 180
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Qy 301 GGGACCAAGGTGGAATTAAG 321
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Db 301 gggaccaagctggaaattaa 321
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ID AAF28178 standard; DNA; 321 BP.
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AC AAF28178;
XX
DT 03-APR-2001 (first entry)
XX
DE Antibody LM609 light chain variable region DNA.
XX
KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 2; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.

XX
SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 82.8%; Score 265.8; DB 22; Length 321;
Best Local Similarity 88.8%; Pred. No. 2.9e-74;
Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;
QY 1 GAGATTGCTAACTAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 60
DB 1 gatattgttaactcagttccagccacccctgtctgtgacaccagagatagcgtcagt 60
QY 61 CTTTCTGCGCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
DB 61 cttctctgcccagccagccaaagtattagcaaccacacacactggtatcaacaaaatca 120
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DB 121 catgagctcccaaggctctccatcagaatcgttccagtcctatctctggatccctcc 180
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RESULT 7
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AC AAZ35244;
XX
XX 13-MAR-2000 (first entry)
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DE Humanised anti-verotoxin II antibody VTml-1 VL cDNA.
XX
KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW monoclonal antibody; light chain; mouse; human; humanised antibody;
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW HUS; therapy; ss.
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OS Homo sapiens.
OS Synthetic.
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XX Key Location/Qualifiers
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FT /*tag= a
FT mat_peptide 61..381
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PN WO9595629-A1.
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XX 25-NOV-1999.
XX
XX 19-MAY-1999; 99WO-US11179.
XX
XX 20-MAY-1998; 98US-0086570.
XX
XX (TEIJ) TEIJIN LTD.
PA (PROT-) PROTEIN DESIGN LABS INC.

XX
PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, CO MS, Vasques M;
XX
XX WPI; 2000-086580/07.
DR P-PSDB; AAY32407.
XX
XX Humanized antibody binding to verotoxin II used for treating Verotoxin
PT producing E. coli -
XX
XX
XX Disclosure; Fig 2b; 59pp; English.
XX
CC This DNA sequence codes for a humanised light chain variable region
CC (see AAY32407) of murine monoclonal antibody VTml-1 (MuVTml-1), an
CC antibody that specifically binds to the B subunit of verotoxin II
CC (VT2). The invention relates to humanised antibodies against VT2
CC that are capable of neutralizing VT2 and/or VT2 variants. The
CC humanised antibody is a humanized form of MuVTml-1 comprising the
CC complementarity determining regions of MuVTml-1 (see AAY32404-05) and
CC heavy and light chain variable region frameworks from the human GF4
CC antibody heavy and light chain frameworks, provided that at least 1
CC position selected from L49, H29, H30, H49 and H98 is occupied by the
CC amino acid at the equivalent position of the MuVTml-1 antibody heavy
CC or light chain variable region framework. Such humanized antibodies
CC have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTml-1.
CC They are used for treating a patient suffering from, or at risk of,
CC the toxic effects from VT2 (claimed), especially for treating
CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic
CC uraemic syndrome (HUS).
XX
SQ Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match 80.5%; Score 258.4; DB 21; Length 381;
Best Local Similarity 87.5%; Pred. No. 6.5e-72;
Matches 280; Conservative 2; Mismatches 38; Indels 0; Gaps 0;
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DB 61 gaaattgtctaaactcagttccagccacccctgtctgtctcaggaagagccact 120
QY 61 CTTTCTGCGCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
DB 121 cttctctgaggccagtcacaaactattagcaacaacacacactggtatcaacaaaacca 180
QY 121 GGTCAAGCCCAAGGCTCTCATCMKKTATCGTTCAGTCCATCTCTGGATCCCGCC 180
DB 181 ggtcaggtcccaaggctctcactcaatcagtcgtctccagtcctatctctggatcccgcc 240
QY 181 AGTTCAGTGGCAGTGATGAGGACAGATTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
DB 241 aggttcagtgccagtgagtcagggacagatttcactctcactatcagcagtcggaatct 300
QY 241 GAGATTTCGAGTCTATTACTGTCAACAGAGTGGCGCTGCACGTTCGGAGG 300
DB 301 gaagatttgcagtgattactgtcaacagagttacagtggtccgcgtccagtcgtgctcaa 360
QY 301 GGGACCAAGCTGGAATTAAG 320
DB 361 gggaccaagctggagatcaa 380
RESULT 8
AAV71800
ID AAV71800 standard; cDNA; 321 BP.
XX
XX AAV71800;
XX
XX 15-MAR-1999 (first entry)
XX
XX Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL cDNA.
XX
XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12HZHC-10; ds.

XX Homo sapiens.
 OS Synthetic.

PN WO9840488-A1.

XX 17-SEP-1998.

PD 12-MAR-1998; 98WO-US04987.

PF 12-MAR-1997; 97US-0039609.

PR (SMIK) SMITHKLINE BEECHAM CORP.

PA Johanson KO, Jonak ZL, Taylor AH;

PI WPI; 1999-034590/03.

DR P-PSDB; AAW84098.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

PS Claim 2; Page 61-62; 97pp; English.

XX This DNA sequence codes for the light chain variable region (VL,
 CC see AAW84098) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence
 CC (see AAW84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions from the murine anti-human
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see
 CC AAW84094). 3 Murine framework residues (1, 49 and 60) are retained
 CC in the synthetic VL. A humanised VH DNA sequence is also provided
 CC (see AAW71799). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 321;
 Best Local Similarity 85.9%; Pred. NO. 2e-69;
 Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCCTCTCTCTCAGCCAGGAGGCGGCT 60

DB 1 gacatagtactgactcagtcctccaggacccctgtcttctccaggagaaagagccacc 60

QY 61 CTTTCTGTCAGCCAGCCGCAAAAGTATTAGCAACCACTTACCTGGTATCAACAAAGGCT 120

DB 61 cttctctgagggccagccaaagattagcaaacacctacactggtatcaacaaacct 120

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKNTAGTTCCTCAGTCCATCTCTGGGATCCCCGCC 180

DB 121 ggcacaggtccgcggctctctcaagtagtcttccagtcctatctctgggtatccctcc 180

QY 181 AGGTTTCAGTGGCAGTGATTCAGGAGGAGGATTCACCCCTACCTATCTCCAGTCTGGGCT 240

XX |||||

DB 181 aggttcagtgccagtgatccaggagacagatttctcactctcaccatcagccgtctagagcct 240

RESULT 9

AAV71802

XX AAV71802 standard; cDNA; 338 BP.

AC AAV71802;

XX 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 MAb VL cDNA.

XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.

XX Mus sp.

OS Synthetic.

XX WO9840488-A1.

PN 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

PR 12-MAR-1997; 97US-0039609.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

DR P-PSDB; AAW84100.

XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Example 13; Page 64; 97pp; English.

XX This DNA sequence codes for the region of the murine monoclonal
 CC antibody (MAb) D12 light chain variable region (VL, see AAW85000)
 CC that is altered in humanised D12 VL (see also AAW84098), including
 CC the first 5 amino acids of the human kappa constant region. It was
 CC prepared from 4 overlapping synthetic oligonucleotides (see
 CC AAV71816-19). The synthetic gene was used to construct an expression
 CC vector for humanised D12 VL. D12 is an anti-alpha-v beta-3
 CC vitronectin receptor MAb. Humanised D12 MAb can be used for
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases.

XX Sequence 338 BP; 82 A; 99 C; 79 G; 78 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 338;
 Best Local Similarity 85.9%; Pred. NO. 2.1e-69;
 Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCCTCTCTCTCAGCCAGGAGGCGGCT 60

```

Db 1 gacatagtactgactcagctccagccacctgtcttctccaggagaagagccacc 60
QY 61 CTTTCTGCGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
Db 61 cttctccgagggcgagcgaagattatagcaaccacctacactggtatcaacaacaccc 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 121 ggccaggctccgcgcttctcatcaagtatgtctccagtcattctctggatccctcc 180
QY 181 AGGTTCAAGTGCAGTGGATCAGGACAGATTCACCTCTACTATCTCCAGCTCGAGCGCT 240
Db 181 aggttcagtgagcagtgagtcagggacagattcactctcaccatcagcgctctagagcct 240
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCGCTTCACACGTTTCGGAGGG 300
Db 241 gaagatttgcggttattactgtcaacagagtaacagctggcctttcaccgttcgagcag 300
QY 301 GGGACCAAGGTGGAATTA 320
Db 301 ggtaccaaggtggaataaa 320

```

RESULT 10

AAQ64167
ID AAQ64167 standard; cDNA to mRNA; 381 BP.

XX AC AAQ64167;

XX DT 29-DEC-1994 (first entry)

XX DE Sequence of mouse V-kappa showing the sequences of recombinant anti-PHV-1 antibody CDRs 1, 2 and 3.

XX KW Feline herpes virus; PHV-1; monoclonal antibody; CDR;
XX RW complementarity determining region; ss.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT CDS 1..381

FT FT /*tag= a

FT FT misc_feature

FT FT 19

FT FT /*tag= b

FT FT /label= MKL104

FT FT misc_feature

FT FT 385..429

FT FT /*tag= c

FT FT /label= MKL124

XX PN WO9412661-A.

XX XX 09-JUN-1994.

XX XX 25-NOV-1993; 93WO-JP01724.

XX XX 28-NOV-1992; 92JP-0341255.

XX XX (KAGA) CHEMO SERO THERAPEUTIC RES INST.

XX XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX XX WPI; 1994-200288/24.

XX XX P-PSDB; AAR54093.

XX XX Feline monoclonal antibody and recombinant antibodies specific for PHV-1 - for detection, treatment and prevention of PHV-1 infection.

XX XX Disclosure; Page 18-19; 53pp; Japanese.

XX XX The inventors claim a monoclonal antibody against feline herpes

XX CC virus (PHV-1). They also claim a recombinant antibody against PHV-1

CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are used in the detection, treatment and prevention of PHV-1. The sequences of the CDRs in the VH of the recombinant anti-PHV-1 antibody are given in AAR54092. The sequences of the CDRs in the VL of the recombinant anti-PHV-1 antibody are given in AAR54093. These CDR sequences are claimed.

XX SQ Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;

Query Match 76.58; Score 245.6; DB 15; Length 381;

Best Local Similarity 85.0%; Pred. No. 7e-68;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCTCAGTCTCCAGCCACCTGTCTCTCAGCCGAGGAGGCGGACT 60

Db 61 gatattgtgctcaactcagctccagccacctgtctgtgactccaggagatagcgtcagt 120

QY 61 CTTTCTGCGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120

Db 121 cttctccgagggcgagcgaagattatagcaacacctacactggtatcaacaacaccc 180

QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTTCCAGTCCATCTCTGGGATCCCGGCC 180

Db 181 catgagttctccaggtctctcatcaagtatgtcttccagtcattctctgggataccctcc 240

QY 181 AGGTTCAAGTGCAGTGGATCAGGACAGATTCACCTCTACTATCTCCAGCTCGAGCGCT 240

Db 241 aggttcagtgagcagtgagtcagggacagattcactctcaccatcagcgctctagagcct 300

QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCGCTTCACACGTTTCGGAGGG 300

Db 301 gaagatttgcggttattactgtcaacagagtaacagctggcctttcaccgttcgagcag 360

QY 301 GGGACCAAGGTGGAATTA 320

Db 361 gggaccaaggtggaataaa 380

RESULT 11

AAF58747

ID AAF58747 standard; cDNA; 381 BP.

XX AC AAF58747;

XX DT 30-APR-2001 (first entry)

XX DE Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.

XX DE ss.

XX DE Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;

XX DE light chain; graft versus host disease; transplant; autoimmune disease;

XX DE multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;

XX DE myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;

XX DE ss.

XX OS Mus sp.

XX XX US6180370-B1.

XX XX 30-JAN-2001.

XX XX 07-JUN-1995; 95US-0484537.

XX XX 28-DEC-1988; 88US-0290975.

XX XX 13-FEB-1989; 89US-0310252.

XX XX 28-SEP-1990; 90US-0590274.

XX XX 19-DEC-1990; 90US-0634278.

XX XX (PROT-) PROTEIN DESIGN LABS INC.

XX XX Queen CL, Selick HE;

XX XX WPI; 2001-190856/19.

XX XX

PN WO9840488-A1.
 XX 17-SEP-1998.
 XX 12-MAR-1998; 98WO-US04987.
 XX 12-MAR-1997; 97US-0039609.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Johanson KO, Jonak ZL, Taylor AH;
 XX WPI; 1999-034590/03.
 DR P-PSDB; AAW84094.
 XX New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX Example 13; Page 59-60; 97pp; English.
 XX This cDNA sequence codes for the light chain variable region (VL,
 CC see AAW84094) of the anti-human alpha-v beta-3 vitronectin receptor
 CC murine monoclonal antibody D12. It was obtained from hybridoma
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers
 CC (see AAV71808-09). A heavy chain variable region clone (see AAV71797)
 CC has also been identified. D12 VH and VL show sequence similarity
 CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
 CC AAW84098) were constructed by combining the framework regions of the
 CC human V region consensus sequences with complementarity determining
 CC regions of D12 (keeping some preferred murine framework residues).
 CC The humanised antibodies are specifically reactive with the human
 CC alpha-v beta-3 protein receptor and capable of neutralising the
 CC receptor. They can be used for passive immunotherapy of a disorder
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 CC disorders or angiogenic-related disorders, such as angiogenesis
 CC associated with diabetic retinopathy, atherosclerosis and
 CC restenosis, chronic inflammatory disorders, macular degeneration,
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
 CC diseases where bone resorption is associated with pathology such as
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone
 CC loss due to immobilisation or sex hormone deficiency. They can also
 CC be used for targeted drug therapy, and for detection and diagnosis.
 XX Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;
 SQ

Query Match 74.5%; Score 239.2; DB 20; Length 324;
 Best Local Similarity 83.88; Pred. No. 6.8e-66;
 Matches 268; Conservative 2; Mismatches 50; Indels 0; Gaps 0;
 QY 1 GAGATTGTCTAAGTCTCCAGCCACCGCTGTCTCAGCCAGGAGAAAGGGCGACT 60
 DB 1 gacattgtctgactcagctccagccacccctgtctgtactccagagatagcgtcagt 60
 QY 61 CTTTCCTGCGCCAGCCAGCAAGTATAGCAACCACTACACTGGTATCAACAAGCCCT 120
 DB 61 ctttcctgcagggccagcagaagattagcaaccacactacactggatcaacaagaatca 120
 QY 121 GGTCACAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGATCCCGGCC 180
 DB 121 catgagctccaagcttctcataagtagcttccagctcactctctggatccctcc 180
 QY 181 AGGTTAGTGCAGTGCATGAGGACAGATTTACCTCTACTATCTCAGTCTGGAGCCT 240
 DB 181 aggttcagagcagtgatcagggacagattctcactctcaatcatcaacattttggagact 240
 QY 241 GAAGATTTTCAGTCTTACTGTCACAGAGTGGCAGCTGGCTCAGACCTTCGGAGGG 300
 DB 241 gaggatttggaaatgtttcttctgcaacagagtaacagctggccttcaacgttcgctcg 300

QY 301 GGGACCAAGGTGGAATTA 320
 DB 301 gggacaaacttggaaataa 320
 RESULT 14
 AAZ35242
 ID AAZ35242 standard; cDNA; 381 BP.
 AC AAZ35242;
 XX 13-MAR-2000 (first entry)
 XX Mouse anti-verotoxin II antibody VTml-1 VL CDNA.
 XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
 KW monoclonal antibody; light chain; mouse; humanised antibody;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
 KW HUS; therapy; ss.
 XX Mus musculus.
 OS
 XX Key Location/Qualifiers
 FT sig_peptide 1..60
 FT mat_peptide /*tag= a
 FT /*tag= b
 FT /transl_except= (pos:184..186, aa:Lys)
 XX WO9959629-A1.
 XX 25-NOV-1999.
 XX 19-MAY-1999; 99WO-US11179.
 XX 20-MAY-1998; 98US-0086570.
 XX (TEIJ) TEIJIN LTD.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
 DR WPI; 2000-086580/07.
 DR P-PSDB; AAY32405.
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli -
 XX Disclosure; Fig 1b; 59pp; English.
 XX This DNA sequence codes for the light chain variable region (see
 CC AAY32405) of murine monoclonal antibody VTml-1 (MuVTml-1), an
 CC antibody that specifically binds to the B subunit of verotoxin II
 CC (VT2). The invention relates to humanised antibodies against VT2
 CC that are capable of neutralizing VT2 and/or VT2 variants. The
 CC humanised antibody is a humanized form of MuVTml-1 comprising the
 CC complementarity determining regions of MuVTml-1 and heavy and
 CC light chain variable region frameworks from the human G4 antibody
 CC heavy and light chain frameworks, provided that at least 1 position
 CC selected from L49, H29, H30, H49 and H98 is occupied by the amino
 CC acid at the equivalent position of the MuVTml-1 antibody heavy or
 CC light chain variable region framework. Such humanised antibodies
 CC (see AAY32405-07) have an affinity for VT2 that is 3-, 5 or 10-times
 CC that of MuVTml-1. They are used for treating a patient suffering
 CC from, or at risk of, the toxic effects from VT2 (claimed), especially
 CC for treating verotoxin producing Escherichia coli (VTEC) infection,
 CC and haemolytic uraemic syndrome (HUS).
 XX Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;
 SQ

Query Match 72.5%; Score 232.8; DB 21; Length 381;

Best Local Similarity 82.5%; Pred. No. 7.4e-64;
Matches 264; Conservative 2; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGATTGCTTAAGTCTCAGCCACCCCTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 61 gatgttgtctaactcagtcctcagccacctgtgtgactccagagatagcgtcagt 120
QY 61 CTTTCCTGCGCAGCCGACCAAGATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
DB 121 ctttctcgagggccagtcataactattagcaacaactacactggtatcaacaataca 180
QY 121 GGTCAAGCCCCAAGGTTCTCATCMKKTAFTGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 catgagtcctcaaggtctctcatcaagtcgtctccagtcctcctggtggtccctcc 240
QY 181 AGGTTTCAGTGGCAGTGGATGAGGAGGAGATTTCCACCTCCTACTATCTCCAGTCTGGAGCCT 240
DB 241 aggttcagtgggcagtggtgagcagatttcactctcagtcacacagtggtggaact 300
QY 241 GAAGATTTCGACGCTTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGGG 300
DB 301 gaagatttggaaatgatttctgtcaacagagttacagctggcgcgtcagcttcgtgct 360
QY 301 GGGACCAAGTGGAAATTA 320
DB 361 gggaccaagctggagctgaa 380

RESULT 15
AAA44346
ID AAA44346 standard; cDNA; 651 BP.
XX
AC AAA44346;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human secreted expressed sequence tag SEQ ID NO:921.
XX
KW Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW thrombolytic; antinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian;
KW antitumor; osteoprotective; neuroprotective; nontropic; antiparasitic;
KW cerebroprotective; anticonvulsant; antidiabetic; gene therapy;
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200021991-A1.
XX
PD 20-APR-2000.
XX
PF 15-OCT-1999; 99WO-US24206.
XX
PR 15-OCT-1998; 98US-0104436.
XX
PA (GEM) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-317938/27.
XX
PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (sESTs), useful for treating various disorders -
PT such as autoimmune, infectious, and central nervous system disorders -

XX
PS
XX
CC AAA43426 to AAA45025 represent specifically claimed secreted expressed
CC sequence tags (sESTs), isolated from human, mouse, chicken and rat
CC tissue sources. The sESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antiasthmatic; vulnary; antitumor; osteopathic; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidiabetic. The sESTs can be used for gene
CC therapy and in vaccines. The sESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;

Query Match 72.1%; Score 231.6; DB 21; Length 651;
Best Local Similarity 82.5%; Pred. No. 2.2e-63;
Matches 264; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 1 GAGATTGCTTAAGTCTCAGCCACCCCTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 94 gacattgtgactcagtcctcagccacctgtgtgactccagagatagctct 153
QY 61 CTTTCCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
DB 154 cttctcgtcagggccagcagagattagcagactactacactggtatcaacaataca 213
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTAFTGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 214 catgagtcctcaaggtctctcatcaaatgcttcccaatcctctctggtatccctcc 273
QY 181 AGGTTTCAGTGGCAGTGGATGAGGAGAGATTTCACCTCCTACTATCTCCAGTCTGGAGCCT 240
DB 274 aggttcagtgagtgatcaggttcagatttcactctcagtcacacagtggtggaacct 333
QY 241 GAAGATTTCAGTCTTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGGG 300
DB 334 gaagatgttggagtgattactgtcaaaaatggtccacagcttccgtcacacgttcggaggg 393
QY 301 GGGACCAAGTGGAAATTA 320
DB 394 gggaccaagctggaaataaa 413

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Job time: 6472 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-08-791-391A-31

Perfect score: 321

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Searched: 324599 seqs, 9465562 residues

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Maximum Match 100%

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	245.6	76.5	381	1	US-07-634-278-82
2	245.6	76.5	381	1	US-08-477-728-82
3	245.6	76.5	381	1	US-08-474-040-82
4	245.6	76.5	381	1	US-08-487-200-82
5	245.6	76.5	381	4	US-08-484-537-82
6	245.6	76.5	424	1	US-08-436-463-3
7	239.6	74.6	5238	6	5453363-1
8	224.8	70.0	321	2	US-08-232-081B-35
9	223.6	69.7	321	2	US-08-232-081B-36
10	222	69.2	324	2	US-08-737-560A-13
11	222	69.2	363	2	US-08-737-560A-8
12	213.6	66.5	322	3	US-08-476-176B-3
13	213.6	66.5	322	3	US-08-127-721A-3
14	213.6	66.5	322	3	US-08-485-246A-3
15	204	63.6	321	2	US-08-232-081B-39
16	201	62.6	318	1	US-08-326-362-3
17	198.8	61.9	318	2	US-08-800-198-3
18	198.8	61.9	318	3	US-09-296-595-3
19	198.8	61.9	720	3	US-08-800-198-7
20	198.8	61.9	720	3	US-09-296-595-7
21	198	61.7	720	2	US-07-956-399-1
22	193.8	60.4	429	2	US-08-653-402B-7
23	191.2	59.6	321	1	US-08-192-102-2
24	191.2	59.6	321	1	US-08-324-799-2
25	191.2	59.6	321	2	US-08-192-861A-2
26	191.2	59.6	717	2	US-07-956-399-3
27	187.2	58.3	812	1	US-08-053-131-178

28	187.2	58.3	812	1	US-08-096-762-178
29	187.2	58.3	812	4	US-09-042-353-41
30	180.8	56.3	900	1	US-08-053-131-180
31	180.8	56.3	900	1	US-08-096-762-180
32	180.8	56.3	900	4	US-09-042-353-43
33	180.4	56.2	931	3	US-09-049-672A-19
34	176.4	55.0	642	2	US-08-480-753-5
35	176.4	55.0	642	3	US-09-041-889-10
36	176.4	55.0	642	3	US-08-837-058-10
37	174.4	54.3	321	4	US-09-240-274-201
38	173.8	54.1	325	5	PCT-US93-12501-1
39	172	53.6	424	2	US-08-476-176B-9
40	172	53.6	424	3	US-08-127-721A-9
41	172	53.6	424	3	US-08-485-246A-9
42	171.8	53.5	321	4	US-09-240-274-216
43	171.2	53.3	321	4	US-09-240-274-107
44	170.8	53.2	321	3	US-08-783-853A-43
45	170.4	53.1	424	2	US-08-476-176B-7

ALIGNMENTS

RESULT 1

US-07-634-278-82

; Sequence 82, Application US/07634278

; Patent No. 5530101

; GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 381 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381.
US-07-634-278-82

Query Match
Best Local Similarity 76.5%; Score 245.6; DB 1; Length 381;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
Db 61 GATATTGTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
QY 61 CTTTCTGCGGAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCT 120
Db 121 CTTTCTGCGGAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCGCC 240
QY 181 AGTTTCAGTGGCAGTGGATCAGGAGCAGATTTACACCCCTCACTATCTCCAGTCTGGAGCT 240
Db 241 AGTTTCAGTGGCAGTGGATCAGGAGCAGATTTACACCCCTCACTATCTCCAGTCTGGAGCT 300
QY 241 GAAGATTTTGGATGTTATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTCCGAGGG 300
Db 301 GAAGATTTTGGATGTTATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTCCGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
Db 361 GGGACCAAGTGGAAATTA 380

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match
Best Local Similarity 76.5%; Score 245.6; DB 1; Length 381;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
Db 61 GATATTGTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
QY 61 CTTTCTGCGGAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCT 120
Db 121 CTTTCTGCGGAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCGCC 240
QY 181 AGTTTCAGTGGCAGTGGATCAGGAGCAGATTTACACCCCTCACTATCTCCAGTCTGGAGCT 240
Db 241 AGTTTCAGTGGCAGTGGATCAGGAGCAGATTTACACCCCTCACTATCTCCAGTCTGGAGCT 300
QY 241 GAAGATTTTGGATGTTATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTCCGAGGG 300
Db 301 GAAGATTTTGGATGTTATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTCCGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
Db 361 GGGACCAAGTGGAAATTA 380

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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Db 241 AGGTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300
QY 241 GAAGATTTTTCAGCTATTACTCTCAACAGAGTGGCCTCACAGCTTCGAGGG 300
Db 301 GAGATTTTGAATGATTTCTCTCAACAGAGTAACAGTTGGCCTCATAGCTTCGAGGG 360
QY 301 GGGACCAAGGTGGAATTA 320
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 5
US-08-484-537-82
; Sequence 82, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELEPHONE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381

US-08-484-537-82

Query Match 76.5%; Score 245.6; DB 4; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.9e-70;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;
QY 1 GAGATTGCTCTAACTCAGTCTCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGACT 60
Db 61 GATATTGCTCTAACTCAGTCTCAGCCACCCCTGCTCTGACTCCGGGAGATAGCGTCACT 120
QY 61 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
Db 121 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 180
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCT 240
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCACTATCTCCAGTCTGGAGCGCT 240
Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTGTCAACCGTGTGGAGACT 300
QY 241 GAAGATTTTTCAGTCTATTACTGTCAACAGAGTGGCCTCACAGCTTCGAGGG 300
Db 301 GAAGATTTTTCAGTCTATTACTGTCAACAGAGTAAACAGTTGGCCTCATAGCTTCGAGGG 360
QY 301 GGGACCAAGGTGGAATTA 320
Db 361 GGGACCAAGCTGGAATAAA 380

RESULT 6
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-EPHILINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE/DOCKET INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 23...403
US-08-436-463-3

Query Match 76.5%; Score 245.6; DB 1; Length 424;
Best Local Similarity 85.0%; Pred. No. 6.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 60
DB 83 GATATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 142
QY 61 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 120
DB 143 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 202
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 203 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 262
QY 181 AGGTTGAGTGCAGTGCAGGAGCAGATTTACACCTTCACTATCTCAGTCTCGAGGCT 240
DB 263 AGGTTGAGTGCAGTGCAGGAGCAGATTTACACCTTCACTATCTCAGTCTCGAGGCT 322
QY 241 GAAGATTTGAGTCTTACTGTCAACAGAGTGGCCTCAGCTTCCAGTCCATCTCTGGGAGG 300
DB 323 GAAGATTTGAGTCTTACTGTCAACAGAGTGGCCTCAGCTTCCAGTCCATCTCTGGGAGG 382
QY 301 GGGACCAAGTGGAAATTA 320
DB 383 GGGACCAAGTGGAGTGA 402

RESULT 7

5453363-1
PATENT NO. 5453363
APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
ING AFTER GENETIC EXPRESSION IN PROKARYOTES
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,044
FILING DATE: 02-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 942,370
FILING DATE: 09-SEP-1992
APPLICATION NUMBER: 498,500
FILING DATE: 23-MAR-1990
APPLICATION NUMBER: 76,207
FILING DATE: 23-OCT-1986
SEQ ID NO: 1
LENGTH: 5238
5453363-1

Query Match 74.6%; Score 239.6; DB 6; Length 5238;
Best Local Similarity 84.1%; Pred. No. 1.5e-67;
Matches 269; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 1 GAGATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 60
DB 7 GATATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 66
QY 61 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 120
DB 67 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 126
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 127 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 186
QY 181 AGGTTGAGTGCAGTGCAGGAGCAGATTTACACCTTCACTATCTCAGTCTCGAGGCT 240

DB 187 AGGTTGAGTGCAGTGCAGGAGCAGATTTCACTCTCAGTATCAACAAGTGGAGCT 246
QY 241 GAAGATTTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 300
DB 247 GAAGATTTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 306
QY 301 GGGACCAAGTGGAAATTA 320
DB 307 GGGACCAAGTGGAGTGA 326

RESULT 8

US-08-232-081B-35
SEQUENCE 35, Application US/08232081B
PATENT NO. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-35

Query Match 70.0%; Score 224.8; DB 2; Length 321;
Best Local Similarity 80.9%; Pred. No. 2.7e-63;
Matches 259; Conservative 2; Mismatches 59; Indels 0; Gaps 0;

QY 1 GAGATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 60
DB 1 GAGATTGCTGTAAGTCTCCAGCAGCCTGCTCTCAGCCAGGAGAGGCGACT 60
QY 61 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 120
DB 61 CTTTCTCCAGGAGCAGCAGCAGTATTAGCAACACCTTACACTGGTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
QY 181 AGGTTGAGTGCAGTGCAGGAGCAGATTTACACCTTCACTATCTCAGTCTCGAGGCT 240

Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTTACTCTTACAATCTCCAGGCTGGAGCCA 240
QY 241 GAAGATTTTGCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 241 GAAGATTTTGCAGTCTATTACTCTCAACAAAGTAGTAGCTGGCCGCTCAGTTTCGGTCAG 300
QY 301 GGGACCAAGGTGGAATAA 320
Db 301 GGGACCAAGGTGAGATAAA 320

RESULT 9
US-08-232-081B-36
; Sequence 36, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIJDNES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-232-081B-36

Query Match 69.7%; Score 223.6; DB 2; Length 321;
Best Local Similarity 80.9%; Pred. No. 6.5e-63;
Matches 259; Conservative 1; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTTGCTTAACCTAGTCTCAGCCACCTGCTCTCAGCCCGAGGAGAAAGGGGACT 60
Db 1 GAGATCGTCTGACTGACTGCTCAGGACACTGTCTCTGAGTCCAGGAGAAAGAGCCACA 60
QY 61 CTTTCTGCGCAGGCGCAAGTATTAGCAACCACTACACTGCTGATCAACAAAGGGCT 120
Db 61 CTGTCTGCGGCGCAGTACAGACCTGTCACCAAGCATACACTGCTATCAGCAGACCA 120
QY 121 GTCAAGCCCCAAGGTTCTTATCMTKKTATCGTTCCTCCAGTCCATCTCTGGGATCCCCGCC 180
Db 121 GCGCAGGCCCCCAAGGTTCTTATATATTATGCTTCTGAGTCTATCTCTGGCATCCCTGAT 180
QY 181 AGGTTTCAGTGGGATCGGATCAGGACAGATTTTCAACCTCACTATCTCCAGTCTGGAGCCT 240

Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTTACTCTTACAATCTCCAGGCTGGAGCCA 240
QY 241 GAAGATTTTGCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 241 GAAGATTTTGCAGTCTATTACTCTCAACAAAGTAGTAGCTGGCCGCTCAGTTTCGGTCAG 300
QY 301 GGGACCAAGGTGGAATAA 320
Db 301 GGGACCAAGGTGAGATAAA 320

RESULT 10
US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuil
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; CITY: Kwanak-gu
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
US-08-737-560A-13

Query Match 69.2%; Score 222; DB 2; Length 324;
Best Local Similarity 80.6%; Pred. No. 2.1e-62;
Matches 258; Conservative 1; Mismatches 61; Indels 0; Gaps 0;

QY 1 GAGATTTGCTTAACCTAGTCTCAGCCACCTGCTCTCAGCCCGAGGAGAAAGGGGACT 60


```

: NAME: No. 5958708ak, Henry P.
: REGISTRATION NUMBER: 33,200
: REFERENCE/DOCKET NUMBER: 4-19276/A/P2/C1P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 277-5110
: TELEFAX: (908) 277-4306
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 322 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..321
: OTHER INFORMATION: /product="light chain
: OTHER INFORMATION: domain of murine antib
US-08-476-176B-3

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Query Match	66.5%;	Score 213.6;	DB 2;	Length 322;
Best Local Similarity	78.8%;	Pred. No. 1.1e-59;		
Matches 252;	Conservative 2;	Mismatches 66;	Indels 0;	Gaps 0;

Qy	1	GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCCTCAGCCCCAGGAGAAGGCGACT	60
Db	1	GACATCTTGCTGACTCAGCTCCAGCCATCTGCTGTGAGTCCAGGAGAAGAGTCAGT	60
Qy	61	CTTTCCTGCCAGGCGAGCCAAAGTATTAGCAACACACCTACACTGGTATCAACAAAGGCT	120
Db	61	TTCTCTGCAGGGCCAGTCAGAGCATTTGGCACAACATACACTGGTATCAGCAAGAACA	120
Qy	121	GGTCAAGCCCCAAGGCTTCTCATCHKTATCGTTCCAGTCCATCTCTGGGATCCCGCC	180
Db	121	GATGGTTCTCCAAAGGCTTCTCATAAAGTATGCTTCTTGAGTCTATCTCTGGGATCCCTCC	180
Qy	181	AGGTTTCAGTGGCAGTGGATCAGGGACAGATTTACCCCTCAGTATCTCCAGTCTGGAGCT	240
Db	181	AGGTTTATAGTGGCAGTGGATCAGGGACAGAGTTTACTCTTAAACATCAACAGTGTGGAGTCT	240
Qy	241	GAAGATTTTGGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTTCACACGTTTCGGAGGG	300
Db	241	GAAGATATTGCAGATTATTACTGTCAACAAAGTGATAGCTGGCCCAACACGTTTCGGAGGG	300
Qy	301	GGGACCAAGGTGGAAATTAA	320
Db	301	GGGACCAAGCTGGAGATAAA	320

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RESULT 13
US-08-127-721A-3
; Sequence 3, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Koibinger, Frank
; APPLICANT: Saidanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127.721A
: FILING DATE: 27-SEPTEMBER-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/952,802
: FILING DATE: 25-SEPTEMBER-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6066718ak, Henry P.
: REGISTRATION NUMBER: 33,200
: REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 277-5110
: TELEFAX: (908) 277-4306
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 322 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..321
: OTHER INFORMATION: /product= "light chain variable
: :
: OTHER INFORMATION: domain of murine antibody TES-C21"
:
: US-08-127-721A-3
:
: Query Match 66.5%; Score 213.6; DB 3; Length 322;
: Best Local Similarity 78.8%; Pred. No. 1.1e-59;
: Matches 252; Conservative 2; Mismatches 66; Indels 0;
:
: QY 1 GAGATTGTCCTAACTCAGCTCTCCAGCCACCCTGCTCTCAGCCCAAGGAGAAAGGGCG
: Db 1 GACATCTTGCTGACTCAGCTCTCCAGCCCACTCTGCTGTGAGTCCAGGAGAAAGAGTCT
: QY 61 CTTTCTCTGCCAGGCGCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAGAG
: Db 61 TTCTCCTCGAGGGCGAGTCAGAGCATTTGGCACAAACATACACTGGTATCAAGCAAGA
: QY 121 GGTCAGCCCAAGGCTTCTATCKTKATCGTTCCCACTCCATCTCTGGGATCCCGA
: Db 121 GATGGTTCTCAAGGCTTCTATAAGTATGCTTCTGAGTCTATCTCTGGGATCCCTT
: QY 181 AGGTTAGTGGCAGTGGATCATGGGACAGATTTACCCCTCACTATCTCCAGTCTGGAG
: Db 181 AGGTTAGTGGCAGTGGATCATGGGACAGAGTTTACTCTAAACATCAACAGTGTGGAG
: QY 241 GAAGATTTGAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTTCGGA
: Db 241 GAAGATATTGAGATTTATTACTGTCAACAAAGATGATAGCTGGCCCAACCCAGTTCGGA
: QY 301 GGGACCAAGTGGAAATTA 320
: Db 301 GGGACCAAGTGGAGATAA 320
:
: RESULT 14
: US-08-485-246A-3
: Sequence 3, Application US/08485246A
: Patent No. 6072035
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 6072035man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saldanha, Jose
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an
: :
: TITLE OF INVENTION: immunoglobulin isotype
: :
: NUMBER OF SEQUENCES: 55
: :
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: NO. 6072035artis Patent Department
: STREET: 59 Route 10
: CITY: East Hanover

```

Query Match	66.5%;	Score	213.6;	DB	3;	Length	322;
Best Local Similarity	78.8%;	Pred. No.	1.1e-59;				
Matches	252;	Conservative	2;	Mismatches	66;	Indels	0;
Gaps	0;						

Qy	1	GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAGGCGAGCT	60
Db	1	GACATCTTGTGACTCAGTCTCCAGCCATCTGTCTGTGAGTCAGGAGAAGAGTCAAGT	60
Qy	61	CTTTCTGCCAGGCGAGCCAAAGTATTAGCAACACCCTACACTGGTATCAACAAGGCGCT	120
Db	61	TTCTCCTGCGAGGCCAGTCAGAGCATTTGGCACAACATACACTGGTATCAACAAGAACA	120
Qy	121	GGTCAAGCCCCAAGGCTTCTCATCMKTKATCGTTGCCAGTCCATCTCTGGGATGCCCGCC	180
Db	121	GATGGTTCTCCAAGGCTTCTCATAAAGTATGCTTCTGTAGTATATCTCTGGGATCCCTTCC	180
Qy	181	AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCAACCCCTCACTATCTCCAGTCTGGAGCCT	240
Db	181	AGGTTTTCAGTGGCAGTGGATCAGGACAGATTTACTCTAAACATCAACAGTGTGGAGTCT	240
Qy	241	GAAGATTTTGCAGTCTATTACTGTCTCAACAGAGTGGCAGCTGGCCTTCACACGTTTCGGAGGG	300
Db	241	GAAGATATTGCAGATTATTACTGTCTCAACAAGTGTAGCTGGCCAAACACCGTTTCGGAGGG	300
Qy	301	GGGACCCAGGTGGAAATTAA	320
Db	301	GGGACCAAGCTGGAGATAAA	320

RESULT 14
US-08-485-246A-3
Sequence 3, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
antigenic epitope of immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover

Job time: 5003 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:36 ; Search time 31.63 Seconds
(without alignments)
257.688 Million cell updates/sec

Title: US-08-791-391a-32
Perfect score: 557
Sequence: 1 EIVLQSPATLSLSPGERAT.....COQSGSWPHTFGGKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	84.4	144	2 PL0106	Ig kappa chain pre
2	460	82.6	111	2 S23628	Ig kappa chain v r
3	458	82.2	128	2 A56701	Ig kappa chain v r
4	457	82.0	128	2 S40379	Ig kappa chain v-j
5	452.5	81.2	114	2 S54905	Ig kappa chain v-j
6	451	81.0	108	2 G44151	Ig kappa chain v r
7	447	80.3	106	2 PC4282	Ig kappa chain (an
8	447	80.3	107	2 B45722	anti-glycoprotein
9	444	79.7	117	2 S40362	Ig kappa chain - h
10	443	79.5	125	2 S40344	Ig kappa chain v-j
11	442	79.4	123	2 S35479	Ig kappa chain pre
12	441	79.2	107	2 A45722	anti-glycoprotein
13	440.5	79.1	109	2 A30608	Ig kappa chain v-i
14	440	79.0	129	2 S29627	Ig kappa chain v r
15	438	78.6	128	2 S40345	Ig kappa chain v-j
16	437	78.5	107	2 S34005	Ig kappa chain v r
17	436	78.3	106	2 PL0267	Ig kappa chain v r
18	433.5	77.8	108	2 B30608	Ig kappa chain v-i
19	433.5	77.8	129	2 A32274	Ig kappa chain pre
20	432.5	77.6	109	2 G30607	Ig kappa chain v-i
21	431.5	77.5	109	1 K3HUTI	Ig kappa chain v-i
22	431	77.4	107	2 S57444	Ig kappa chain v-j
23	430.5	77.3	109	2 D30601	Ig kappa chain v-i
24	430.5	77.3	109	2 C30601	Ig kappa chain v-i
25	429.5	77.1	109	2 H30601	Ig kappa chain v-i
26	429	77.0	128	2 S40343	Ig kappa chain v-j
27	428.5	76.9	109	1 K3HUSI	Ig kappa chain v-i
28	427.5	76.8	109	2 G30601	Ig kappa chain v-i
29	427.5	76.8	109	2 B30601	Ig kappa chain v-i

30	427.5	76.8	128	2 S20636	Ig kappa chain v r
31	427.5	76.8	129	1 K3HUAH	Ig kappa chain pre
32	426.5	76.6	215	2 JE0244	Ig kappa chain NIG
33	425.5	76.4	108	2 C30608	Ig kappa chain v-i
34	424.5	76.2	110	2 S20635	Ig kappa chain v r
35	424.5	76.2	129	2 S49532	anti-sm antibody v
36	423.5	76.0	109	2 PH0663	Ig kappa chain v r
37	423.5	76.0	109	2 F30607	Ig kappa chain v-i
38	422.5	75.9	109	1 K3HWWL	Ig kappa chain v-i
39	422.5	75.9	129	1 K3HUIH	Ig kappa chain pre
40	420	75.4	114	2 S46375	Ig kappa chain v-j
41	419.5	75.3	130	2 S40360	Ig kappa chain - h
42	419	75.2	138	2 A26471	Ig kappa chain pre
43	417.5	75.0	43	2 F30601	Ig kappa chain v-i
44	417.5	75.0	129	2 S46369	Ig light chain var
45	417.5	75.0	134	2 S38643	Ig kappa chain v r

ALIGNMENTS

RESULT 1

PL0106

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PL0106

R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PL0106; MUID:89235583

A:Accession: PL0106

A:Molecule type: mRNA

A:Residues: 1-144 <SIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match 84.4%; Score 470; DB 2; Length 144;

Best Local Similarity 85.0%; Pred. No. 1.4e-34;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSLSCASQSIHNLHWYQORPGQAPRLLIYRSQSTSGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSLSCASQSVSYLAWYQORPGQAPRLLIYDSNRATGIPA 80

Qy 61 RFSGSGGTDTFTLTSSLEPEDFAVYVYCCQSGSWPHTFGGKTRVEIK 107

Db 81 RFSGSGGTDTFTLTSSLEPEDFAVYVYCCQSRNPNLTFGGKTRVEIK 127

RESULT 2

S23628

Ig kappa chain v region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23628

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804

A:Accession: S23628

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>

QY 64 GSGSGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 63 GSGSGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 106

RESULT 7

PC4282
Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
A:Reference number: PC4279; MUID:97236289
A:Accession: PC4282
A:Molecule type: protein
A:Residues: 1-106 <SUZ>
A:Note: E-42
A:Molecule type: protein
A:Accession: PC4284
A:Residues: 1-106 <SUZ>
A:Note: E-56
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjog
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 106;
Best Local Similarity 81.0%; Pred. No. 1.1e-32;
Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYXSQISGIPARF 62
|||||
Db 1 VLTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYDISKRATGIPAKF 60

QY 63 SGSGSGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 SGSGSGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 105

RESULT 8

B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833
A:Accession: B45722
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 107;
Best Local Similarity 75.7%; Pred. No. 1.1e-32;
Matches 81; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYXSQISGIPA 60
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Db 1 DIVLTQSPATLSVTPGDSVLSLSCAQSISNHLHWYQQRPGQAPRLLIYKASQISGIP 60

QY 61 RFSGSGGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 61 RFSGSGGTDTLTINSVETEDFGVFCQQTNSWPHTFGGKLEIK 107

RESULT 9

S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 444; DB 2; Length 117;
Best Local Similarity 79.4%; Pred. No. 2.2e-32;
Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYXSQISGIPA 60
|||||
Db 11 EIVLTQSPATLSVSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYGASTRATGIPA 70

QY 61 RFSGSGGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
|||||
Db 71 RFSGSGGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 117

RESULT 10

S40344
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40344
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40344
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72454; NID:9441376; PIDN:CAA51122.1; PID:9441377
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 443; DB 2; Length 125;
Best Local Similarity 81.9%; Pred. No. 2.8e-32;
Matches 86; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYXSQISGIPA 60
:|||||
Db 21 EVLVTQSPATLSLSPGERATLSCAQSISNHLHWYQQRPGQAPRLLIYDASNRATGIPA 80

QY 61 RFSGSGGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 105
|||||
Db 81 RFSGSGGTDTLTISLEPEFAVYVYCOQSGSWPHTFGGKVEIK 125

RESULT 11

S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 442; DB 2; Length 123;
Best Local Similarity 74.8%; Pred. No. 3.4e-32;
Matches 80; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60
Db 13 DIVLTQSPATLSVTPGDKVSLSCRASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPS 72
QY 61 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 107
Db 73 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 119

RESULT 12
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBI:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 441; DB 2; Length 107;
Best Local Similarity 73.8%; Pred. No. 3.6e-32;
Matches 79; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60
Db 1 DIVLTQSPATLSVTPGDKVSLSCRASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPS 60
QY 61 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 107
Db 61 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 107

RESULT 13
A30608
Ig kappa chain V-III region (Son) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: A30608
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989

A:Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A:Reference number: A30601; MUID:89215279
A:Accession: A30608
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 440.5; DB 2; Length 109;
Best Local Similarity 81.5%; Pred. No. 4.1e-32;
Matches 88; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 59
Db 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 60
QY 60 ARFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 107
Db 61 NFRSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 108

RESULT 14
S29627
Ig kappa chain V region (60.3 hybridoma) - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34110; S29627
R:Walls, M.A.; Hsiao, K.; Harris, L.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
A:Reference number: S34110; MUID:93324379
A:Accession: S34110
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <WAS>

A:Cross-references: EMBL:Z17330; NID:38511; PIDN:CAA78978.1; PID:g38512
A:Note: human sequences cloned and sequenced prior to expression in mouse myeloma cel
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 440; DB 2; Length 129;
Best Local Similarity 79.8%; Pred. No. 5.3e-32;
Matches 87; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 80
QY 61 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 107
Db 81 RFSGSGSGTDFTLTISLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 129

RESULT 15
S40345
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40345
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40345
A:Status: preliminary; translation not shown

A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PID:g441379
C:Superfamily: immunoglobulin v region; immunoglobulin Homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 438; DB 2; Length 128;
Best Local Similarity 78.9%; Pred. No. 7.9e-32;
Matches 86; Conservative 8; Mismatches 13; Indels 2; Gaps 1;
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISGNHLHWYQORPGQAPRLLIYXRQSISGIPA 60
Db 17 EIVLTQSPATLSLSPGERATLSCQASQISGNHLHWYQORPGQAPRLLIYXRQSISGIPA 60
QY 61 RFSGSGSGTDFTLTISLEPEDFAVYYCQOSGSPH--TFGGGTKVEIK 107
Db 77 RFSGSGSGTDFTLTISLEPEDFAVYYCQOSGSPH--TFGGGTKVEIK 125

Search completed: October 11, 2001, 12:02:36
Job time: 301 sec

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PLO021; K3HUHI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 75.9%; Score 422.5; DB 1; Length 129;
Best Local Similarity 79.6%; Pred. No. 3.4e-37;
Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 59
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYGASSRATGIP 80
Qy 60 ARFSGSGGTDFTLTISLLEPDAFYVYCOQSGSPHPTFGGKVEIK 107
Db 81 DRFSGSGGTDFTLTISLLEPDAFYVYCOQSGSPHPTFGGKVEIK 128

RESULT 6
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DE 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CIL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorce J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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DR EMBL; M12740; AAA58992.1; -.
DR PIR; A01898; K3HUC1.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 5C13B411BE60CC14 CRC64;

Query Match 75.1%; Score 418.5; DB 1; Length 129;
Best Local Similarity 75.9%; Pred. No. 8.7e-37;
Matches 82; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 80
Qy 61 RFSGSGGTDFTLTISLLEPDAFYVYCOQSGSW-PHTFGGKVEIK 107
Db 81 RFSGSGGTDFTLTISLLEPDAFYVYCOQYNNWPPWTFGQGRVEIK 128

RESULT 7
KV3I_HUMAN STANDARD; PRT; 115 AA.
ID KV3I_HUMAN
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DE 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01568; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUV.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RM Milstein C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies
 of Bence Jones proteins Rad, Fr4 and B6.";
 RL FEBS Lett. 2:301-304(1969).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01891; K3HUB6.
 DR HSP; P01789; 2MCP.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT TSULFID 23
 FT NON_TER 108 108
 FT SEQUENCE 108 AA; 8BC14FF07A419E3D CRC64;
 QY Query Match 73.0%; Score 406.5; DB 1; Length 108;
 Best Local Similarity 73.1%; Pred. No. 1.3e-35;
 Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;
 QY 1 EIVLTQSPATLSLSPGERATLSCAQSIS-NHLHWYQQRCPQAPRLLIYRSQSISGIP 59
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 ZIVLTZSPGTLSPGZRAALSCRASQSLCNLAWYQKCPQAPRLLMYGVSSRATGIP 60
 QY 60 ARFGSGSGDTFTLTISLPEDFAVYYCQSGSWPHTFGGTVK 107
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 DRFGSGSGADFTLTISRLZPEDFAVYYCQYSGSPFTFGGSKLEIK 108
 RESULT 10
 KV3K_HUMAN STANDARD; PRT; 128 AA.
 ID KV3K_HUMAN
 AC P06311;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 R Klobbeck H.G., Meindl A., Combiato G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 III.";
 RL Nucleic Acids Res. 13:6499-6513(1985).
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 CC EMBL; Z00021; CAA77316.1; -.
 DR PIR; A01899; K3HU41.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 128
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 FT DOMAIN 55 69
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 FT DOMAIN 2404 2416
 FT DOMAIN 2417 2429
 FT

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FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.9%; Score 406; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 1.7e-35;
Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQTSIGIPA 60
DB 21 EIVLTQSPGTLSPGESATLSQASQSVSNLAWYQKRGQSPRLLIYRSQTSIGIPA 80
QY 61 RFSGSGSGTDFTLTISLLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 81 RFSGSGSGTDFTLTISLLEPEFAVYVYCOQYSTSPYTFGGKLEIK 127

RESULT 11
KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies."
RL Mol. Immunol. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
DR Immunoglobulin V region.
KW DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11630 MW; 9349A5B1D9358B6 CRC64;

Query Match 72.3%; Score 402.5; DB 1; Length 109;
Best Local Similarity 75.9%; Pred. No. 3.3e-35;
Matches 82; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQTSIGIP 59
DB 1 EIVLTQSPGTLSPGERATLSQAAALSSRGYLAQYQKPGQAPRLLIYRSQTSIGIP 60
QY 60 ARFSGSGSGTDFTLTISLLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 DRFSGSGSGTDFTLTISLLEPEFAVYVYCOQYSPRSGFGGKVEIK 108

RESULT 12
KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK 1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 56 FRAMEWORK 2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 68.2%; Score 380; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 7.1e-33;
Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQTSIGIPA 60
DB 1 DIQMTQSPSSLSVSGVDRVTITCQASQNVNAYLNWYQKPKLIIYGASTREAGVPS 60
QY 61 RFSGSGSGTDFTLTISLLEPEFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 RFSGSGSGTDFTLTISLLOPEADIATYVCOQVNNWPPTEGGGKVEIK 107

RESULT 13
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01868; K1HULH.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
```


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Result No.	Query No.	Score	%		Length	DB	ID	Description
			Match					
1	429.5	77.1	109	4	Q9UL85	Q9UL85 homo sapien		
2	428	76.8	108	4	Q9UL83	Q9UL83 homo sapien		
3	427.5	76.8	109	4	Q9UL78	Q9UL78 homo sapien		
4	402.5	72.3	109	4	Q9UL86	Q9UL86 homo sapien		
5	385	69.1	108	4	Q9UL77	Q9UL77 homo sapien		
6	372	66.8	108	4	Q9UL79	Q9UL79 homo sapien		
7	366	65.7	108	4	Q9UL70	Q9UL70 homo sapien		
8	362.5	65.1	107	4	Q9UL81	Q9UL81 homo sapien		
9	338.5	60.8	106	5	Q9UL10	Q9UL10 schistosoma		
10	334	60.0	99	11	Q9JL74	Q9JL74 mus musculus		
11	334	60.0	107	11	Q9JL84	Q9JL84 mus musculus		
12	332	59.6	298	11	Q9JF0	Q9JF0 mus musculus		
13	331	59.4	214	11	Q9RIA5	Q9RIA5 mus musculus		
14	326	58.5	101	11	Q9JL78	Q9JL78 mus musculus		
15	315	56.6	107	11	Q9EZ9	Q9EZ9 mus musculus		
16	314	56.4	103	11	Q9JL80	Q9JL80 mus musculus		
17	309	55.5	97	11	Q9JL76	Q9JL76 mus musculus		
18	309	55.5	114	4	Q9UL80	Q9UL80 homo sapien		
19	307.5	55.2	104	11	Q9JL82	Q9JL82 mus musculus		

01-MAY-2000 (TREMBlrel. 13, Created)
01-MAY-2000 (TREMBlrel. 13, Last sequence update)
01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 69.1%; Score 385; DB 4; Length 108;
Best Local Similarity 69.2%; Pred. NO. 7e-36;
Matches 74; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPQAPRLLIYRQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISLNYLWYQQKPKAPRLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITSSLEPEDFAYVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFGSGSGTDFLTITSSLOPEDFAYVYCOQSYSTSWTFGGKVEIK 107

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79;
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 66.8%; Score 372; DB 4; Length 108;
Best Local Similarity 67.3%; Pred. NO. 2e-34; 21; Indels 0; Gaps 0;
Matches 72; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPQAPRLLIYRQSISGIPA 60
Db 1 DIVMTQSPSLLSASTGDRVITTCRMSQGISLNYLWYQQKPKAPRLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITSSLEPEDFAYVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFGSGSGTDFLTITSSLOPEDFAYVYCOQYYSFPPTFGGKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 65.7%; Score 366; DB 4; Length 108;
Best Local Similarity 64.5%; Pred. NO. 9.5e-34;
Matches 69; Conservative 17; Mismatches 21; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPQAPRLLIYRQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISLNYLWYQQKPKAPRLLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITSSLEPEDFAYVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFGSGSGTDFLTITSSLOPEDFAYVYCOKYNAPRTFGGKLEIK 107

RESULT 8
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:58 ; Search time 44.8 Seconds
(without alignments)
144.794 Million cell updates/sec

Title: US-08-791-391a-32

Perfect score: 557

Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHFGGTRKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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 - 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
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 - 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
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 - 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	99.6	107	19 AAW76006	LM609 grafted anti
2	555	99.6	107	19 AAW76002	Vitaxin antibody 1
3	555	99.6	107	22 AAB61360	Vitaxin light chal
4	555	99.6	107	22 AAB61364	Light chain variab
5	506	90.8	107	13 AAR25729	Humanised VL regio
6	506	90.8	107	22 AAB69678	Humanised CMV5 ant
7	506	90.8	107	22 AAB69690	Human Wol antibody
8	504	90.5	107	20 AAW84098	Humanised anti-alp
9	504	90.5	112	20 AAW84100	Vitronectin alpha-
10	501	89.9	127	18 AAW08946	Kappa light chain
11	495	88.9	107	18 AAW08948	Kappa light chain

12	495	88.9	107	18	AAW08949	Kappa light chain
13	490	88.0	107	20	AAV30205	The variable light
14	489	87.8	107	20	AAV30203	The variable light
15	484	86.9	127	21	AAV32407	Mouse anti-verotox
16	480	86.2	127	15	AAR50192	Light chain variab
17	480	86.2	127	20	AAV26982	Light chain variab
18	478	85.8	107	14	AAR37612	hIL2R Ab L chain V
19	477	85.6	107	21	AAV71240	Humanised antibody
20	474	85.1	107	21	AAV70604	Vkappa region of h
21	474	85.1	127	15	AAR50187	Light chain variab
22	474	85.1	127	20	AAV26980	Light chain variab
23	474	85.1	245	21	AAV70605	scfv fragment of h
24	471	84.6	127	15	AAR50191	Light chain variab
25	471	84.6	127	20	AAV26981	Light chain variab
26	464	83.3	107	19	AAV76004	LM609 antibody lig
27	464	83.3	107	22	AAB61362	Antibody LM609 lig
28	455	81.7	107	22	AAB66414	Human Fab clone LD
29	453	81.3	107	21	AAV71238	Humanised antibody
30	450.5	80.9	108	22	AAB72884	Human anti-HER2/ne
31	450	80.8	105	20	AAW87456	Jk gene product.
32	450	80.8	105	20	AAW87458	Humanised anti-alp
33	449.5	80.7	107	18	AAW24513	Anti-Factor-IX hum
34	449	80.6	109	20	AAV06380	Murine monoclonal
35	446	80.1	214	20	AAV08599	Anti-human TNF-alp
36	441	79.2	107	22	AAB69677	Murine CMV5 antibo
37	441	79.2	127	22	AAB69687	Murine CMV5 antibo
38	440	79.0	349	12	AAR12128	1B1 IgG aberrant 1
39	440	79.0	401	12	AAR12129	ORF 1 of IgG light
40	440	79.0	414	12	AAR13111	1B1 IgG aberrant 1
41	440	79.0	414	12	AAR13018	1B1 IgG aberrant 1
42	438.5	78.7	109	22	AAB62756	Human HIV-1 monocl
43	438	78.6	127	15	AAR54093	Sequence of mouse
44	436.5	78.4	108	21	AAV53774	VL component of an
45	436.5	78.4	238	21	AAV53775	An antibody with i

ALIGNMENTS

RESULT 1

AAW76006
ID AAW76006 standard; Protein; 107 AA.

XX AAW76006;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.

OS Mus sp.

XX Key Location/Qualifiers

FT Misc-difference 49

FT /label= Arg, Met

XX WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX XX

DR WPI; 1998-437472/37.
 DR N-PSDB; AAV49843.
 XX
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 19; Fig 7; 129pp; English.
 XX
 CC This sequence represents a LM609 grafted antibody variable light chain
 CC region. LM609 and the antibody vitaxin bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 107 AA;
 SQ

Query Match 99.6%; Score 555; DB 19; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60
 QY 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGTRKEIK 107
 DB 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGTRKEIK 107
 DB 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGTRKEIK 107

RESULT 2
 AAW76002
 ID AAW76002 standard; Protein; 107 AA.
 XX
 AC AAW76002;
 XX
 XX 02-NOV-1998 (first entry)
 DT
 XX Vitaxin antibody light chain variable region protein fragment.
 DE
 XX
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 XX
 XX Mus sp.
 OS
 XX WO9833919-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US01826.
 PF
 XX 30-JAN-1997; 97US-0791391.
 PR
 XX (IXSY-) IXSYS INC.
 PA
 XX Glaser SM, Huse WD;
 PI
 XX WPI; 1998-437472/37.
 DR N-PSDB; AAV49821.
 DR
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 XX
 XX Claim 1; Fig 1b; 129pp; English.
 XX
 CC This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 XX
 XX Sequence 107 AA;
 SQ

Query Match 99.6%; Score 555; DB 19; Length 107;
 Best Local Similarity 99.1%; Pred. No. 3.7e-36;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60
 QY 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGTRKEIK 107
 DB 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGTRKEIK 107

RESULT 3
 AAB61360
 ID AAB61360 standard; protein; 107 AA.
 XX
 AC AAB61360;
 XX
 XX 03-APR-2001 (first entry)
 DT
 XX Vitaxin light chain variable region protein.
 DE
 XX
 XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.
 KW
 XX Unidentified.
 OS
 XX WO200078815-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 23-JUN-2000; 2000WO-US17454.
 PF
 XX 24-JUN-1999; 99US-0339922.
 PR
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Huse WD, Wu H;
 PI
 XX WPI; 2001-050110/06.
 DR
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -
 XX
 XX Disclosure; Fig 1; 132pp; English.
 PS
 XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphavbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.
 XX
 SQ Sequence 107 AA;

Query Match 99.6%; Score 555; DB 22; Length 107;
 Best Local Similarity 99.1%; Pred. No. 3.7e-36;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60
 QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQSGSWPHTFGGKVEIK 107
 DB 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQSGSWPHTFGGKVEIK 107

RESULT 4

AAB61364
 ID AAB61364 standard; protein; 107 AA.

XX AAB61364;

DT 03-APR-2001 (first entry)

DE Light chain variable region of LM609.

KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

OS Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 PT osteoporosis -

PS Disclosure; Fig 7; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or
 CC their functional fragments. The antibodies or their functional
 CC fragments can be used in the diagnosis and treatment of
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory
 CC diseases (such as psoriasis and chronic articular rheumatism),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
 CC diseases (such as macular degeneration), restenosis and
 CC osteoporosis.

XX Sequence 107 AA;

Query Match 99.6%; Score 555; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60
 QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQSGSWPHTFGGKVEIK 107
 DB 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQSGSWPHTFGGKVEIK 107

RESULT 5

AAR25729
 ID AAR25729 standard; Protein; 107 AA.

XX AAR25729;

DT 13-JAN-1993 (first entry)

DE Humanised VL region of the mouse CMV5 antibody.

KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW GH; light chain; variable region; framework; human; Wol.

OS Mus musculus.

XX Key Location/Qualifiers

FT Region 24..34

FT /note= "CDR"

FT Region 50..56

FT /note= "CDR"

FT Region 89..97

FT /note= "CDR"

FT Misc-difference 49

FT /note= "mutated residue"

XX WO9211018-A.

XX 09-JUL-1992.

XX 19-DEC-1991; 91WO-US09711.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;

XX WPI; 1992-249842/30.

XX New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions

XX Claim 40; Fig 27A; 141pp; English.

XX The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the GH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also AAR25721-32.

XX

QY 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQSGSWPHTFGGGKVEIK 107
 |||||
 Db 61 rfsgsgsgtdftltisrlepedfavyycqsgswphftfgggtkveik 107

RESULT 8

AAW84098
 ID AAW84098 standard; Protein; 107 AA.

XX AC AAW84098;

XX DT 15-MAR-1999 (first entry)

XX DE Humanised anti-alpha-v beta-3 Mab D12H2HC 1-0 VL.

XX KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 D12H2HC-10.

XX OS Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers
 XX Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX DR N-PSDB; AAV71800.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX FS Claim 2; Page 61-62; 97pp; English.

XX This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
 CC (see AAW84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions (CDRs) from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60)
 CC are retained. The humanised light chain can be expressed in host
 CC cells using nucleic acid molecules (see AAV71800) of the invention.
 CC Humanised D12 VH is also provided (see AAW84097). The humanised
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
 CC angiogenic-related disorders, such as angiogenesis associated
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone
 CC resorption is associated with pathology such as osteoporosis,

CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.

XX SQ Sequence 107 AA;

Query Match 90.5%; Score 504; DB 20; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3,1e-32;
 Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQRPQAPRLILXYRQSISGIPA 60
 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
 Db 1 divltqspgtlsispgeratlsqrasqisnlhwyqkpgqaprlilkyasqsigips 60

QY 61 RFSGSGSGTDFLTITSSLEPEDFAVYYCQSGSWPHTFGGGKVEIK 107
 |||||

Db 61 rfsgsgsgtdftltisrlepedfavyycqsgswphftfgggtkveik 107
 |||||

RESULT 9

AAW84100
 ID AAW84100 standard; Protein; 112 AA.

XX AC AAW84100;

XX DT 15-MAR-1999 (first entry)

XX DE Vitronectin alpha-v beta-3 Mab VL.

XX KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX DR N-PSDB; AAV71802.

XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX Example 13; Page 64; 97pp; English.

XX This is the amino acid sequence of the region of the murine
 CC monoclonal antibody (Mab) D12 light chain variable region (VL)
 CC that is altered in humanised D12 VL (see also AAW84098). A
 CC synthetic gene (see AAW81902) encoding the protein was prepared
 CC from synthetic oligonucleotides and used to prepare an expression
 CC vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3
 CC vitronectin receptor Mab. Humanised D12 Mabs can be used for
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases.

SQ Sequence 107 AA;

Query Match 88.9%; Score 495; DB 18; Length 107;
 Best Local Similarity 87.9%; Pred. No. 1.5e-31;
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60
 |||||
 Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60
 |||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
 |||||
 Db 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
 |||||

RESULT 12
 AAW08949
 ID AAW08949 standard; Protein; 107 AA.
 XX
 AC AAW08949;
 XX
 DT 18-SEP-1997 (first entry)
 XX
 DE Kappa light chain variable region of 225RB antibody.
 XX
 KW Kappa; light chain; reshaped; monoclonal; antibody; 225RB;
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KW tumour; cell; late stage; prostatic; prostate; variable region;
 KW framework; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Region 1..23
 FT /label= framework_1
 FT Region 24..34
 FT /label= CDR_1
 FT Region 35..49
 FT /label= framework_2
 FT Region 50..56
 FT /label= CDR_2
 FT Region 57..88
 FT /label= framework_3
 FT Region 89..97
 FT /label= CDR_3
 FT Region 98..107
 FT /label= framework_4
 XX
 PN WO9640210-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09847.
 XX
 PR 15-DEC-1995; 95US-0573289.
 PR 07-JUN-1995; 95US-0482982.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (MRCC-) MRC COLLABORATIVE CENT.
 XX
 PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;
 XX
 DR WPI; 1997-051897/05.
 XX
 PT Chimeric and humanised versions of anti-EGF receptor antibody 225 -
 PT used for inhibiting tumour growth, esp. of late stage prostatic
 PT tumour
 XX
 PS Claim 29; Fig 21; 112pp; English.
 XX
 CC The present sequence is the kappa light chain variable region
 CC of the reshaped human monoclonal antibody (MAB) H225, 225RKA. The

CC MAB is specific for the human epidermal growth factor (EGF)
 CC receptor.
 CC The MAB, or a fragment, can be used to inhibit the growth of tumour
 CC cells, especially late stage prostatic tumour cells in humans,
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle
 CC inhibitor.
 XX
 SQ Sequence 107 AA;

Query Match 88.9%; Score 495; DB 18; Length 107;
 Best Local Similarity 87.9%; Pred. No. 1.5e-31;
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60
 |||||
 Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60
 |||||

QY 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
 |||||
 Db 61 RFGSGSGTDFLTITSSLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
 |||||

RESULT 13
 AAY30205
 ID AAY30205 standard; Protein; 107 AA.
 XX
 AC AAY30205;
 XX
 DT 01-NOV-1999 (first entry)
 XX
 DE The variable light chain of humanised antibody L3.17.
 XX
 KW Light chain variable region; chimeric antibody; anti-CD40 antibody;
 KW chi220; humoral immune response; T cell dependent antigen;
 KW collagen induced arthritis; transplant induced rejection;
 KW T cell mediated disorder; autoimmune disease; inflammatory disease;
 KW transplantation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9942075-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 10-FEB-1999; 99WO-US02949.
 XX
 PR 19-FEB-1998; 98US-0026291.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;
 PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
 XX
 DR WPI; 1999-527408/44.
 DR N-PSDB; AAZ10205.
 XX
 PT Antibody that binds human CD40, for treating T cell mediated
 PT disorders
 XX
 PS Claim 26; Page 33-34; 77pp; English.
 XX
 CC The present sequence represents the variable light chain of humanised
 CC antibody L3.17. The antibody is effective in modulating humoral immune
 CC response against T cell dependent antigens, collagen induced arthritis
 CC and transplant induced rejection. They are also useful for their
 CC anti-inflammatory properties. The antibodies have wide therapeutic
 CC applications, including autoimmune and inflammatory diseases and
 CC transplantation. The antibody can be used in a pharmaceutical composition
 CC for treating a patient suffering from a T cell mediated disorder. They
 CC can also be used to treat autoimmune diseases, inflammatory diseases,

CC and transplantation.

XX Sequence 107 AA;

Query Match

88.0%; Score 490; DB 20; Length 107;

Best Local Similarity 88.8%; Pred. No. 3.7e-31;

Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQISNHLHWYQORPGAPRLIIXYRSOSISGIPA 60

Db 1 eivltqspatlsispggeratlsragsisdylhwyqkpgqprllyiyashsisgipa 60

QY 61 RFGSGSGDTFTLTISLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107

Db 61 rfgsgsgdtftltislslepedfavyccqghghsfptwtfgggtkveik 107

RESULT 14

AAV3203

ID AAY30203 standard; Protein; 107 AA.

XX

AC AAY30203;

XX 01-NOV-1999 (first entry)

DT

XX The variable light chain of humanised antibody F4.

DE

XX Light chain variable region; chimeric antibody; anti-CD40 antibody;

KW chi220; humoral immune response; T cell dependent antigen;

KW collagen induced arthritis; transplant induced rejection;

KW T cell mediated disorder; autoimmune disease; inflammatory disease;

KW transplantation.

XX Synthetic.

OS Homo sapiens.

XX WO942075-A2.

PN 26-AUG-1999.

XX 10-FEB-1999; 99WO-US02949.

PF 19-FEB-1998; 98US-0026291.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;

PI Huse WD, Sladak AW, Thorne BA, Watkins JD, Wu H;

XX WPI; 1999-527408/44.

DR N-PSDB; AA210203.

XX Antibody that binds human CD40, for treating T cell mediated

PT disorders

XX Claim 21; Page 32-33; 77pp; English.

XX The present sequence represents the variable light chain of humanised

CC antibody F4. The antibody is effective in modulating humoral immune

CC response against T cell dependent antigens, collagen induced arthritis

CC and transplant induced rejection. They are also useful for their

CC anti-inflammatory properties. The antibodies have wide therapeutic

CC applications, including autoimmune and inflammatory diseases and

CC transplantation. The antibody can be used in a pharmaceutical composition

CC for treating a patient suffering from a T cell mediated disorder. They

CC can also be used to treat autoimmune diseases, inflammatory diseases,

CC and transplantation.

XX Sequence 107 AA;

Query Match

87.8%; Score 489; DB 20; Length 107;

Best Local Similarity 88.8%; Pred. No. 4.4e-31;

Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQISNHLHWYQORPGAPRLIIXYRSOSISGIPA 60

Db 1 eivltqspatlsispggeratlsragsisdylhwyqkpgqprllyiyashsisgipa 60

QY 61 RFGSGSGDTFTLTISLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107

Db 61 rfgsgsgdtftltislslepedfavyccqghghsfptwtfgggtkveik 107

RESULT 15

AAV32407

ID AAY32407 standard; Protein; 127 AA.

XX

AC AAY32407;

XX

XX 13-MAR-2000 (first entry)

DT

XX Mouse anti-verotoxin II antibody Vtm1-1 humanised VL region.

DE

XX Verotoxin II; VT2; shiga-like toxin; Vtm1-1; MuVtm1-1;

KW monoclonal antibody; light chain; mouse; humanised antibody; human;

KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;

KW HUS; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

FT Peptide

FT /note= "signal peptide"

FT Protein

FT /note= "mature protein"

FT Region

FT /note= "complementarity determining region 1"

FT Region

FT /note= "complementarity determining region 2"

FT Region

FT /note= "complementarity determining region 3"

FT

XX WO959629-A1.

PN 25-NOV-1999.

XX 19-MAY-1999; 99WO-US11179.

XX 20-MAY-1998; 98US-0086570.

PR (TEIJ) TEIJIN LTD.

PA (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;

XX WPI; 2000-086580/07.

DR N-PSDB; AA235244.

XX Humanized antibody binding to verotoxin II used for treating Verotoxin

PT producing E. coli

XX Claim 12; Fig 2b; 59pp; English.

XX This sequence represents a humanised light chain variable region of

CC murine monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that

CC specifically binds to the B subunit of verotoxin II (VT2). The

CC invention relates to humanised antibodies against VT2 that are capable

CC of neutralizing VT2 and/or VT2 variants. The humanised antibody is a

CC humanized form of MuVtm1-1 comprising the complementarity determining

CC regions of MuVtm1-1 and the heavy and light chain variable region

CC frameworks from the human GP4 antibody heavy and light chain

CC frameworks, provided that at least 1 position selected from L49, H29,

CC H30, H49 and H98 is occupied by the amino acid at the equivalent

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GenCore version 4.5
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OM protein - protein search, using sw.model
Run on: October 11, 2001, 12:06:42 ; Search time 239.24 seconds
(without alignments)
99.221 Million cell updates/sec

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Perfect score: 557
Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQGSWPHFTGGTRVETK 107

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Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues
Total number of hits satisfying chosen parameters: 2803329

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Listing first 45 summaries

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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	99.6	107	US-08-790-540-4	Sequence 4, Appli
2	555	99.6	107	US-08-790-540A-4	Sequence 4, Appli
3	555	99.6	107	US-08-791-391-4	Sequence 4, Appli
4	555	99.6	107	US-08-791-391-32	Sequence 32, Appli
5	555	99.6	107	US-08-791-391A-4	Sequence 4, Appli
6	555	99.6	107	US-08-791-391A-32	Sequence 32, Appli
7	555	99.6	107	US-09-016-061-4	Sequence 4, Appli
8	555	99.6	107	US-09-016-061-32	Sequence 32, Appli
9	555	99.6	107	US-09-339-922A-4	Sequence 4, Appli
10	555	99.6	107	US-09-339-922A-32	Sequence 32, Appli

11	506	90.8	107	17	US-09-325-000-22	Sequence 22, Appli
12	504	90.5	107	1	PCT-US98-04987-10	Sequence 10, Appli
13	504	90.5	107	17	US-09-380-910-10	Sequence 10, Appli
14	504	90.5	112	1	PCT-US98-04987-14	Sequence 14, Appli
15	504	90.5	112	17	US-09-380-910-14	Sequence 14, Appli
16	501	89.9	127	13	US-08-973-065A-17	Sequence 17, Appli
17	501	89.9	127	13	US-08-973-065B-17	Sequence 17, Appli
18	495	88.9	107	13	US-08-973-065B-114	Sequence 114, Appli
19	490	88.0	107	1	PCT-US99-02949-12	Sequence 12, Appli
20	490	88.0	107	14	US-09-026-291-12	Sequence 12, Appli
21	490	88.0	107	16	US-09-247-352-12	Sequence 12, Appli
22	489	87.8	107	1	PCT-US99-02949-8	Sequence 8, Appli
23	489	87.8	107	14	US-09-026-291-8	Sequence 8, Appli
24	489	87.8	107	16	US-09-247-352-8	Sequence 8, Appli
25	483	86.7	107	13	US-08-973-065B-113	Sequence 113, Appli
26	482	86.5	113	13	US-08-973-065A-22	Sequence 22, Appli
27	482	86.5	113	13	US-08-973-065A-23	Sequence 23, Appli
28	482	86.5	113	13	US-08-973-065B-22	Sequence 22, Appli
29	482	86.5	113	13	US-08-973-065B-23	Sequence 23, Appli
30	480	86.2	127	5	US-08-127-721-10	Sequence 10, Appli
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32	480	86.2	127	8	US-08-485-246-10	Sequence 10, Appli
33	478	85.8	107	6	US-08-232-081-9	Sequence 9, Appli
34	478	85.8	107	6	US-08-232-081A-9	Sequence 9, Appli
35	477	85.6	107	18	US-09-438-954-3	Sequence 3, Appli
36	474	85.1	107	1	PCT-US99-21646-25	Sequence 25, Appli
37	474	85.1	107	17	US-09-397-569-25	Sequence 25, Appli
38	474	85.1	127	5	US-08-127-721-6	Sequence 6, Appli
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45	471	84.6	127	8	US-08-485-246-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-790-540-4
; Sequence 4, Application US/08790540
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; STREET: Campbell & Flores LLP
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,540
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

RESULT 10
US-09-339-922A-32
; Sequence 32, Application US/09339922A
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (49)
; OTHER INFORMATION: Xaa - Arg or Met
; OTHER INFORMATION: Description of Artificial Sequence: grafted
; OTHER INFORMATION: antibody variable region
US-09-339-922A-32

Query Match 99.6%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRQSISGIPA 60
QY 61 RFSGSGGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107
DB 61 RFSGSGGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 11
US-09-325-000-22
; Sequence 22, Application US/09325000
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coeligh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252

; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-325-000-22

Query Match 90.8%; Score 506; DB 17; Length 107;
Best Local Similarity 90.7%; Pred. No. 6e-44;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRQSISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRQSISGIPD 60
QY 61 RFSGSGGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107
DB 61 RFSGSGGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 12
PCT-US98-04987-10
; Sequence 10, Application PC/TUS9804987
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04987
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/039,609
; FILING DATE: 12 March 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: P50629-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4800
TELEFAX: 610-270-4026
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US98-04987-10

Query Match 90.5%; Score 504; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 9.7e-44;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60
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Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIYASQSIGIPS 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
QY 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGNSWPTFGGKTVEIK 107

RESULT 13
US-09-380-910-10
; Sequence 10, Application US/09380910
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; Jonak, Zdenka L.
; Taylor, Alexander H.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,910
; FILING DATE: 24-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/039,609
; FILING DATE: 12 March 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: P50629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-380-910-10

Query Match 90.5%; Score 504; DB 17; Length 107;
Best Local Similarity 89.7%; Pred. No. 9.7e-44;

Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIYASQSIGIPS 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
QY 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107
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Db 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGNSWPTFGGKTVEIK 107

RESULT 14
PCT-US98-04987-14
; Sequence 14, Application PC/TUS9804987
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04987
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/039,609
; FILING DATE: 12 March 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T.
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: P50629-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4800
; TELEFAX: 610-270-4026
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US98-04987-14

Query Match 90.5%; Score 504; DB 1; Length 112;
Best Local Similarity 89.7%; Pred. No. 1e-43;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIYASQSIGIPS 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
QY 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
Db 61 RFSGSGGTDTLTISLEPEDFAVYCCQSGNSWPTFGGKTVEIK 107

RESULT 15
US-09-380-910-14
; Sequence 14, Application US/09380910
; GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation
Jonak, Zdenka L.
Johanson, Kyung O.
Taylor, Alexander H.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,910
FILING DATE: 24-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/039,609
FILING DATE: 12 March 1997
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: P50629
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-380-910-14

Query Match 90.5%; Score 504; DB 17; Length 112;
Best Local Similarity 89.7%; Pred. No. 1e-43;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLILYRSQSISGIPA 60
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
1 DIVLTQSPGTLTLSPGERATLSCRASQISNHLHWYQRPQAPRLILYRSQSISGIPS 60
QY 61 RFGSGSGTDFLTITSLLEPEDFAVYCCQSGSWPHTFGGPKVEIK 107
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
61 RFGSGSGTDFLTITSLRLEPEDFAVYCCQSGNSWPFTEGGPKVEIK 107

Search completed: October 11, 2001, 12:06:42
Job time: 397 sec

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